

FIG. 1

SUBSTITUTE SHEET

53

RELATIVE
NUMBER
OF CELLS

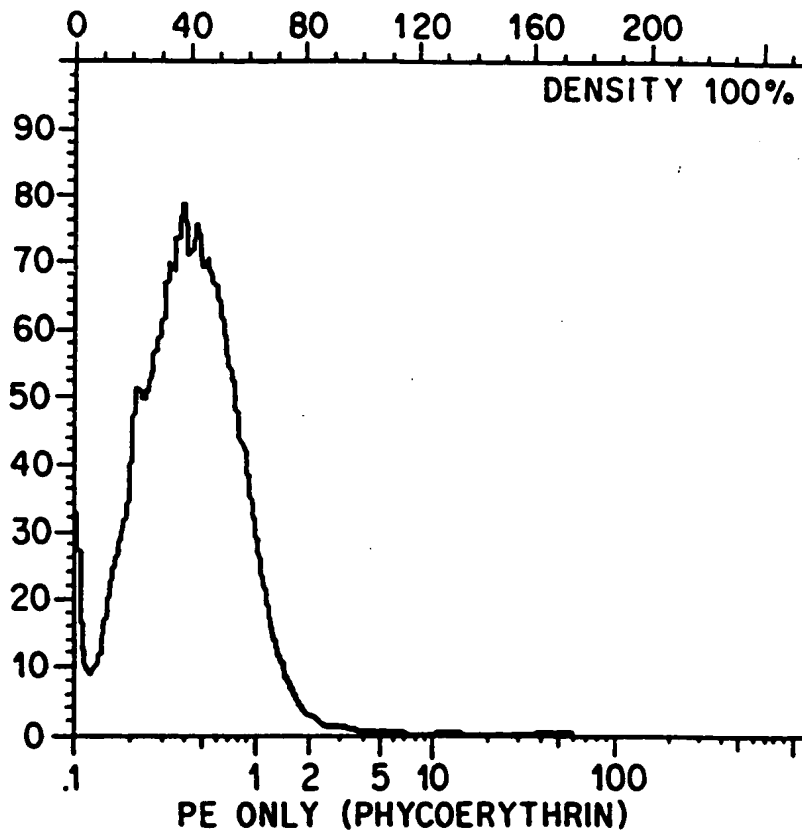


FIG. 2A

RELATIVE
NUMBER
OF CELLS

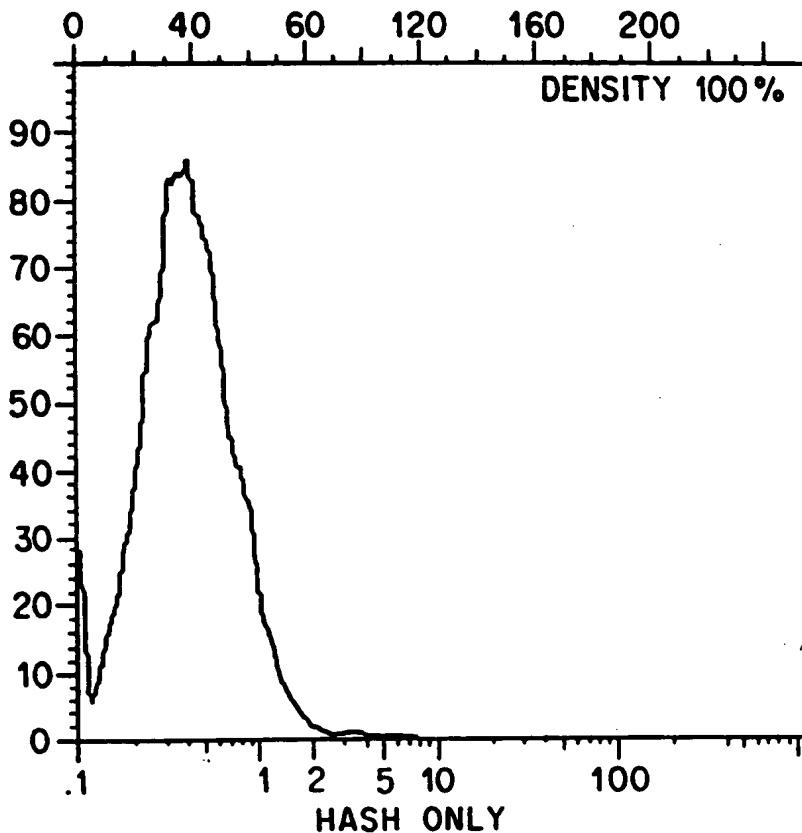


FIG. 2B

SUBSTITUTE SHEET

RELATIVE
NUMBER
OF CELLS

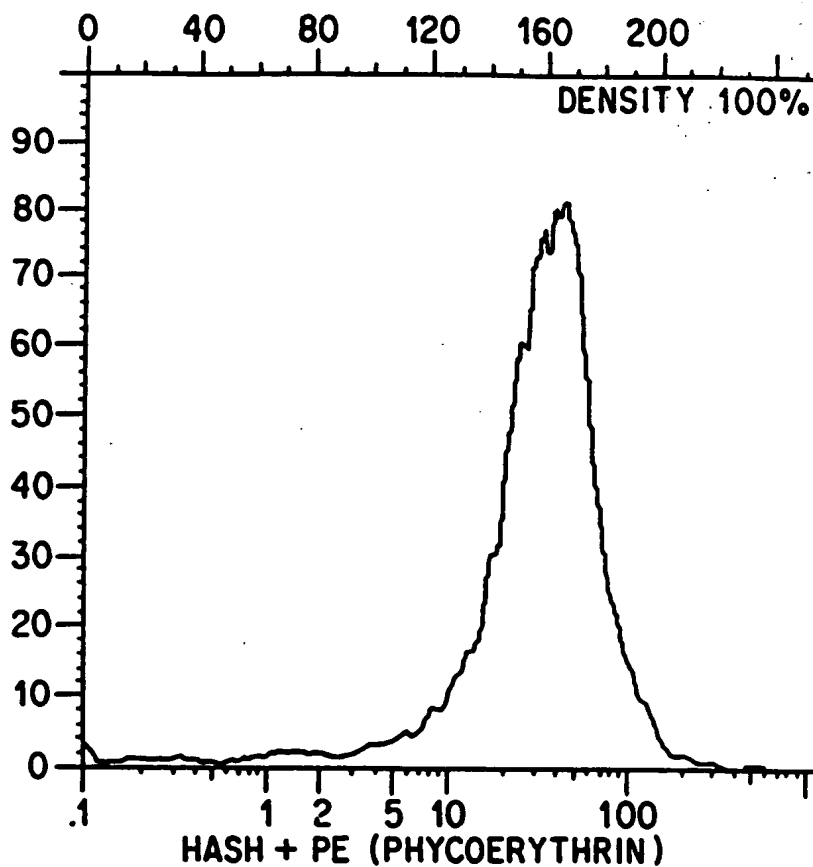


FIG. 2C

RELATIVE
NUMBER
OF CELLS

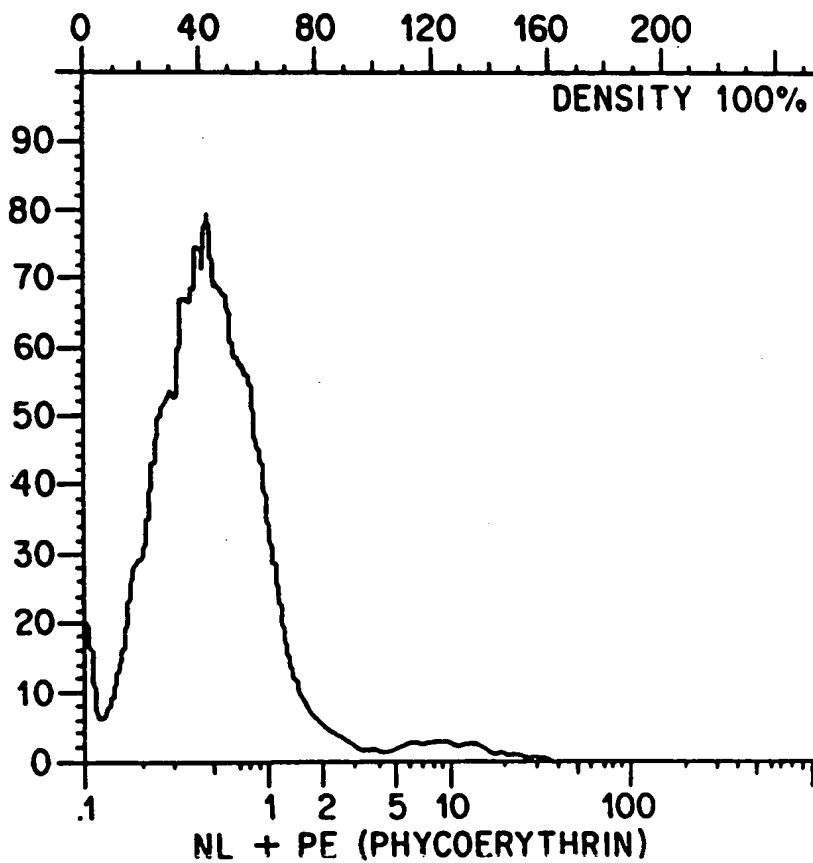


FIG. 2D

HASH + PE
(PHYCOERYTHRIN)

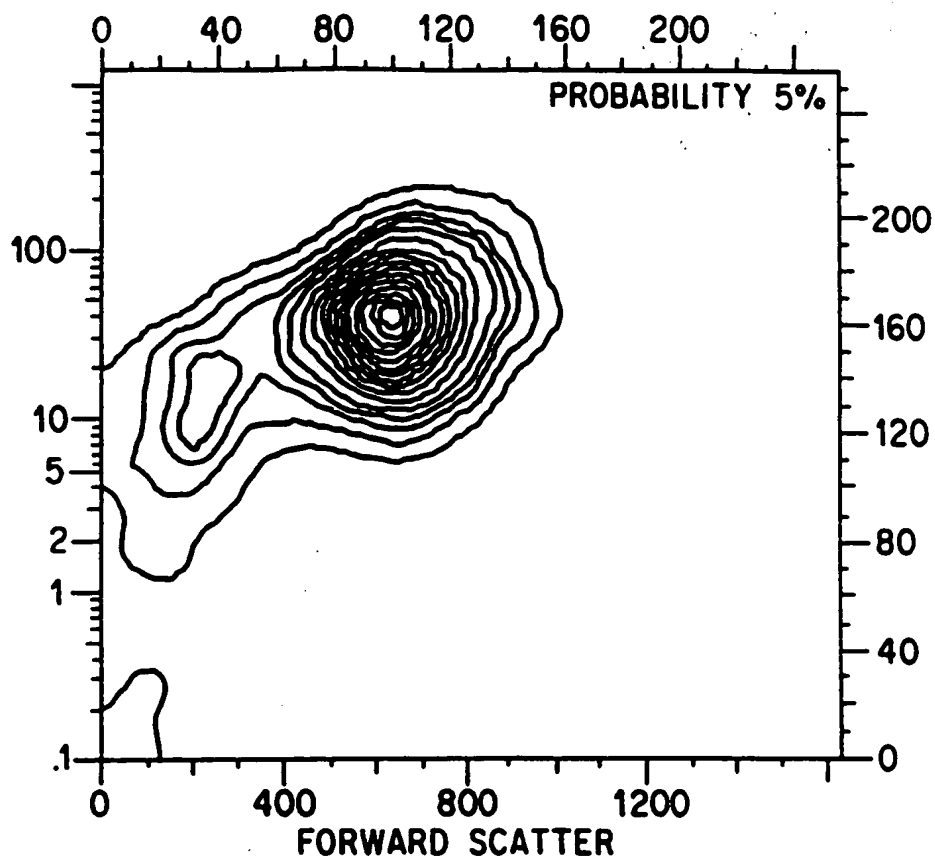


FIG. 2E

NL + PE
(PHYCOERYTHRIN)

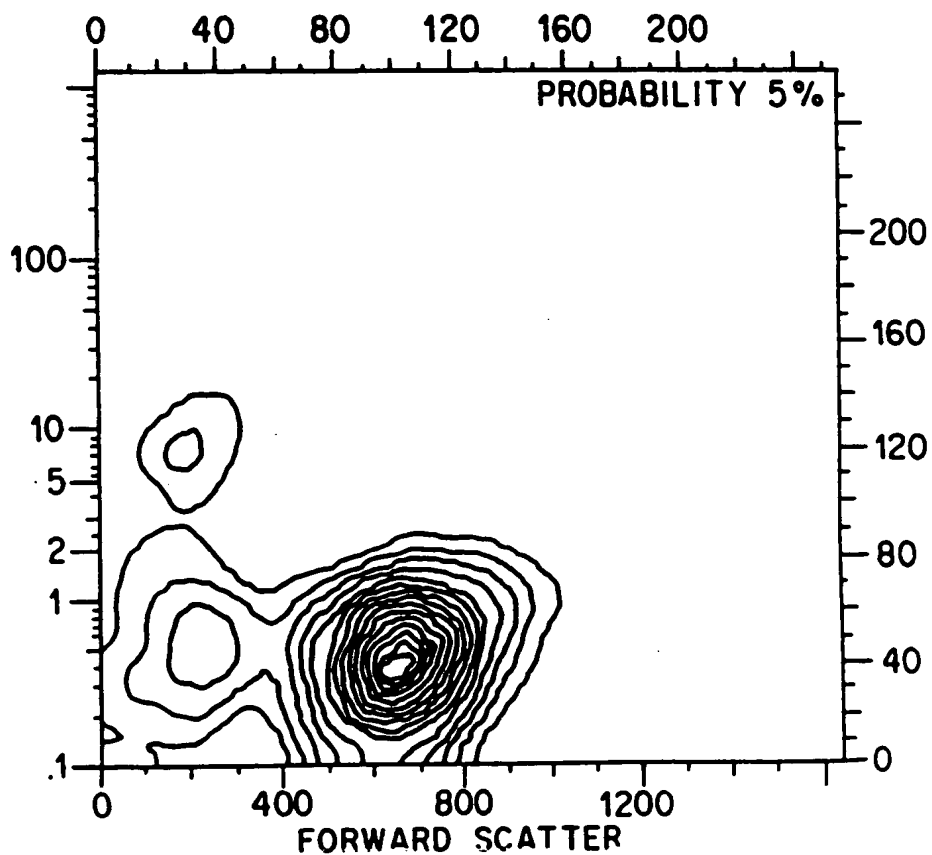


FIG. 2F

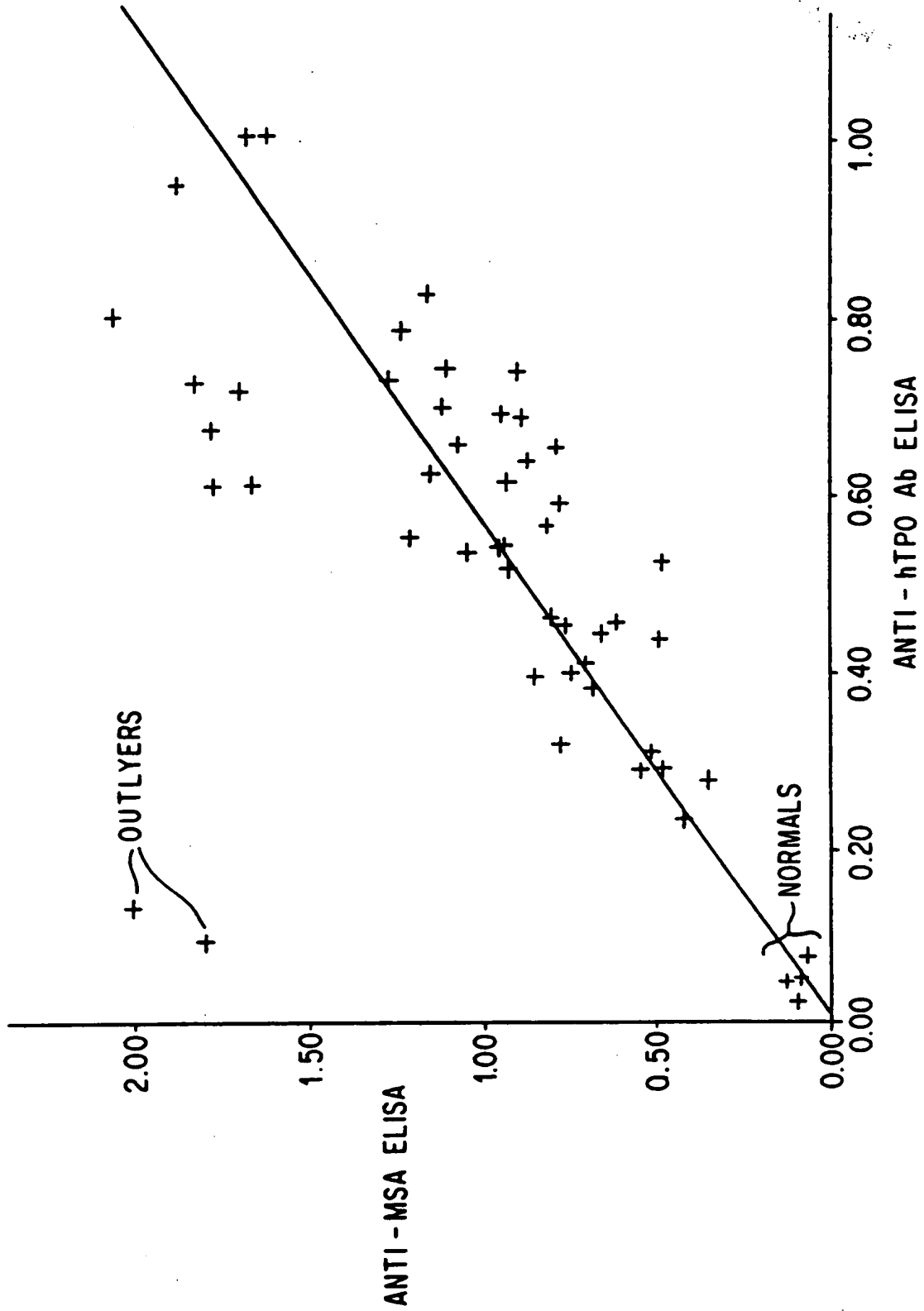


FIG. 3

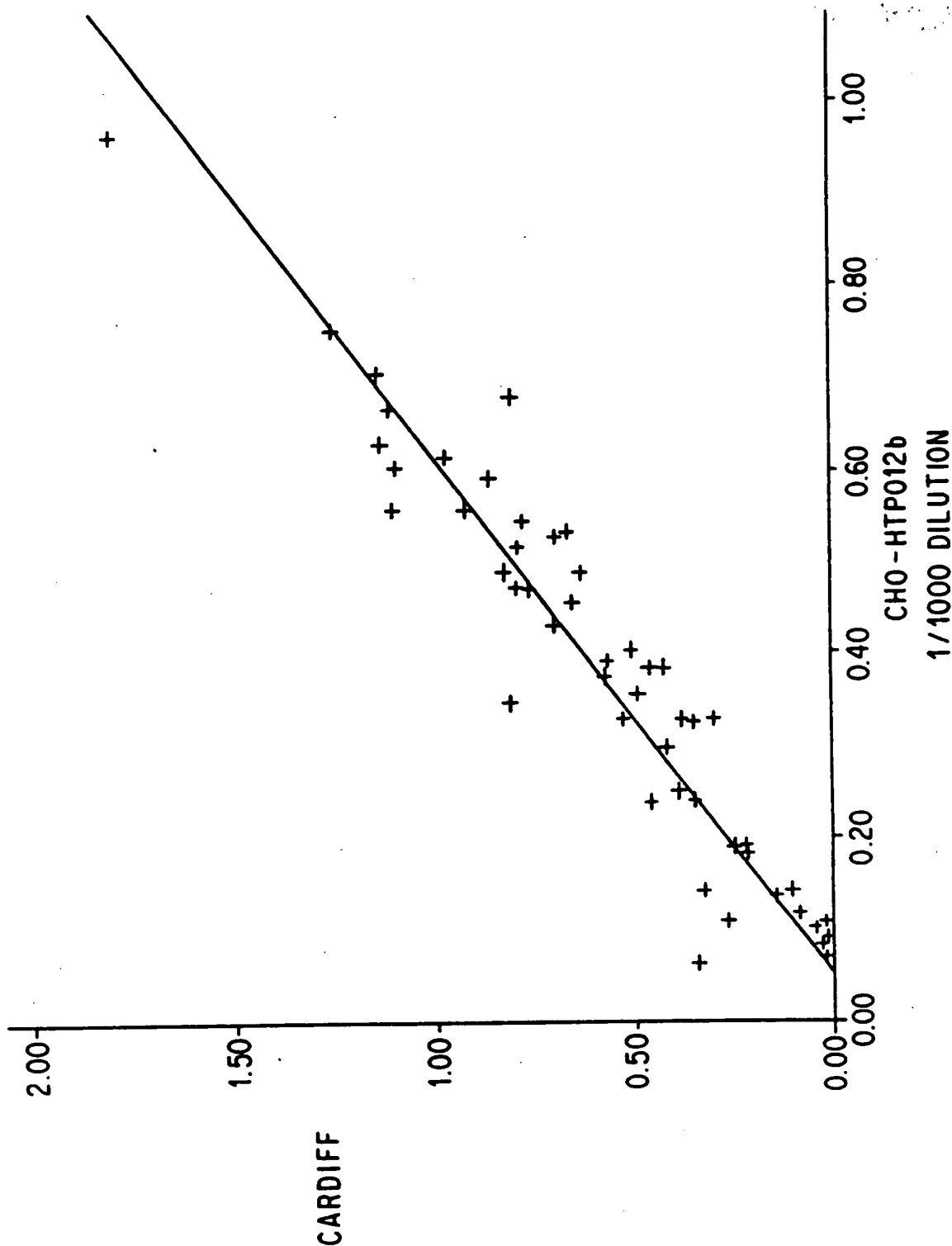


FIG. 4

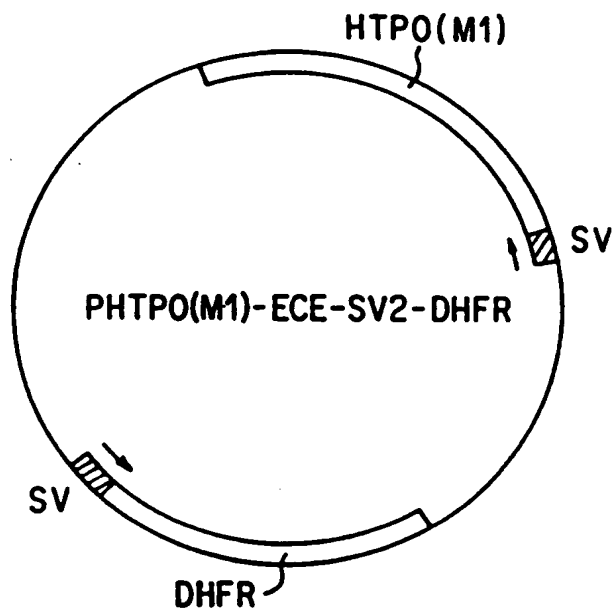


FIG. 8

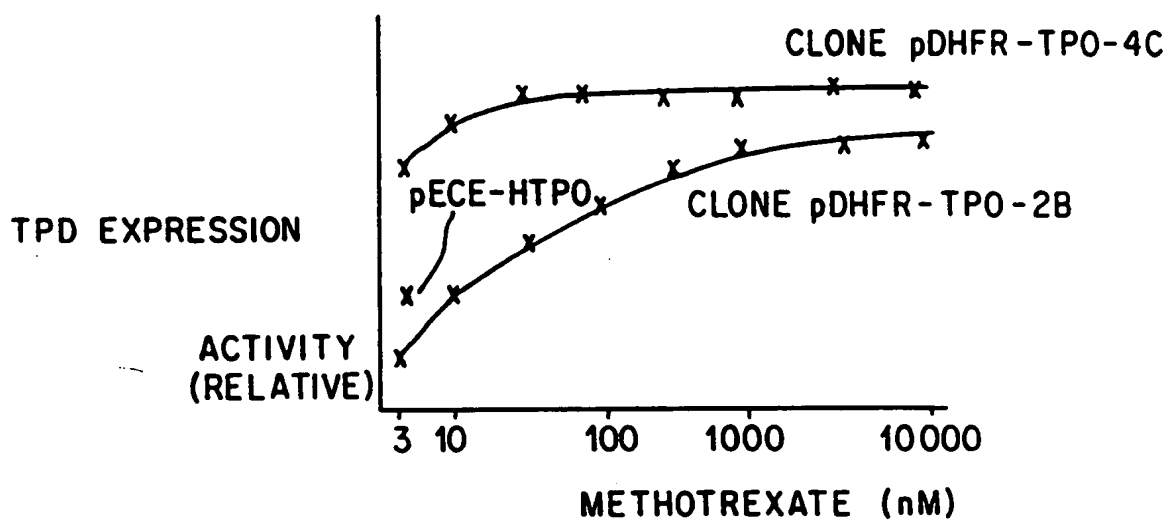


FIG. 5

SUBSTITUTE SHEET

2611
 AGG CTC CCT CGG GTG ACT TGG ATC ICC ATG TCG CIG GCT GCT CIG CIG ATC G PHTPD-BS
 2662

Eco RI

Stop

Stop

AGG CTC CCT CGG GTG ACT TGA ATT CCC ATG TAG CIG GCT GCT CIG CIG ATC G PHTPD(MI)-BS

FIG. 6

SUBSTITUTE SHEET

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27	54
GAG GCA ATT GAG GCG CCC ATT TCA GAA GAG TTA CAG CCG TGA AAA TTA CTC AGC	
81	108
AGT GCA GTT GGC TGA GAA GAG GAA AAA AGA ATG AGA GCG CTG GCT GTG CTG TCT	
	MET Arg Ala Leu Ala Val Leu Ser
135	162
GTC ACG CTG GTT ATG GCC TGC ACA GAA GCC TTC TTC CCC TTC ATC TCG AGA GGG	
Val Thr Leu Val Met Ala Cys Thr Glu Ala Phe Phe Pro Phe Ile Ser Arg Gly	
189	216
AAA GAA CTC CTT TGG GGA AAG CCT GAG GAG TCT CGT GTC TCT AGC GTC TTG GAG	
Lys Glu Leu Leu Trp Gly Lys Pro Glu Glu Ser Arg Val Ser Ser Val Leu Glu	
243	270
GAA AGC AAG CGC CTG GTG GAC ACC GCC ATG TAC GCC ACG ATG CAG AGA AAC CTC	
Glu Ser Lys Arg Leu Val Asp Thr Ala Met Tyr Ala Thr Met Gln Arg Asn Leu	
297	324
AAG AAA AGA GGA ATC CTT TCT GGA GCT CAG CTT CTG TCT TTT TCC AAA CTT CCT	
Lys Lys Arg Gly Ile Leu Ser Gly Ala Gln Leu Leu Ser Phe Ser Lys Leu Pro	
351	378
GAG CCA ACA AGC GGA GTG ATT GCC CGA GCA GCA GAG ATA ATG GAA ACA TCA ATA	
Glu Pro Thr Ser Gly Val Ile Ala Arg Ala Ala Glu Ile Met Glu Thr Ser Ile	
405	432
CAA GCG ATG AAA AGA AAA GTC AAC CTG AAA ACT CAA CAA TCA CAG CAT CCA ACG	
Gln Ala Met Lys Arg Lys Val Asn Leu Lys Thr Gln Gln Ser Gln His Pro Thr	
459	486
GAT GCT TTA TCA GAA GAT CTG CTG AGC ATC ATT GCA AAC ATG TCT GGA TGT CTC	
Asp Ala Leu Ser Glu Asp Leu Leu Ser Ile Ile Ala Asn Met Ser Gly Cys Leu	

x

FIG. 7A**SUBSTITUTE SHEET**

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	513	540
CCT TAC ATG CTG CCC CCA AAA TGC CCA AAC ACT TGC CTG GCG AAC AAA TAC AGG		
Pro Tyr Met Leu Pro Pro Lys Cys Pro Asn Thr Cys Leu Ala Asn Lys Tyr Arg		
	567	594
CCC ATC ACA GGA GCT TGC AAC AAC AGA GAC CAC CCC AGA TGG GGC GCC TCC AAC		
Pro Ile Thr Gly Ala Cys Asn Asn Arg Asp His Pro Arg Trp Gly Ala Ser Asn		
	621	648
ACG GCC CTG GCA CGA TGG CTC CCT CCA GTC TAT GAG GAC GGC TTC AGT CAG CCC		
Thr Ala Leu Ala Arg Trp Leu Pro Pro Val Tyr Glu Asp Gly Phe Ser Gln Pro		
	675	702
CGA GGC TGG AAC CCC GGC TTC TTG TAC AAC GGG TTC CCA CTG CCC CCG GTC CGG		
Arg Gly Trp Asn Pro Gly Phe Leu Tyr Asn Gly Phe Pro Leu Pro Pro Val Arg		
	729	756
GAG GTG ACA AGA CAT GTC ATT CAA GTT TCA AAT GAG GTT GTC ACA GAT GAT GAC		
Glu Val Thr Arg His Val Ile Gln Val Ser Asn Glu Val Val Thr Asp Asp Asp		
	783	810
CGC TAT TCT GAC CTC CTG ATG GCA TGG GGA CAA TAC ATC GAC CAC GAC ATC GCG		
Arg Tyr Ser Asp Leu Leu MET Ala Trp Gly Gln Tyr Ile Asp His Asp Ile Ala		
	837	864
TTC ACA CCA CAG AGC ACC AGC AAA GCT GCC TTC GGG GGA GGG TCT GAC TGC CAG		
Phe Thr Pro Gln Ser Thr Ser Lys Ala Ala Phe Gly Gly Gly Ser Asp Cys Gln		
	891	918
ATG ACT TGT GAG AAC CAA AAC CCA TGT TTT CCC ATA CAA CTC CCG GAG GAG GCC		
Met Thr Cys Glu Asn Gln Asn Pro Cys Phe Pro Ile Gln Leu Pro Glu Glu Ala		
	945	972
CGG CCG GCC GCG GGC ACC GCC TGT CTG CCC TTC TAC CGC TCT TCG GCC GCC TGC		
Arg Pro Ala Ala Gly Thr Ala Cys Leu Pro Phe Tyr Arg Ser Ser Ala Ala Cys		

FIG. 7B**SUBSTITUTE SHEET**

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999 1026
 GGC ACC GGG GAC CAA GGC GCG CTC TTT GGG AAC CTG TCC ACG GCC AAC CCG AGG
 Gly Thr Gly Asp Gln Gly Ala Leu Phe Gly Asn Leu Ser Thr Ala Asn Pro Arg

*

1053 1080
 CAG CAG ATG AAC GGG TTG ACC TCG TTC CTG GAC GCG TCC ACC GTG TAT GGC AGC
 Gln Gln Met Asn Gly Leu Thr Ser Phe Leu Asp Ala Ser Thr Val Tyr Gly Ser

1107 1134
 TCC CCG GCC CTA GAG AGG CAG CTG CGG AAC TGG ACC AGT GCC GAA GGG CTG CTC
 Ser Pro Ala Leu Glu Arg Gln Leu Arg Asn Trp Thr Ser Ala Glu Gly Leu Leu

*

1161 1188
 CGC GTC CAC GGC CGC CTC CGG GAC TCC GGC CGC GCC TAC CTG CCC TTC GTG CCG
 Arg Val His Gly Arg Leu Arg Asp Ser Gly Arg Ala Tyr Leu Pro Phe Val Pro

1215 1242
 CCA CGC GCG CCT GCG GCC TGT GCG CCC GAG CCC GGC AAC CCC GGA GAG ACC CGC
 Pro Arg Ala Pro Ala Ala Cys Ala Pro Glu Pro Gly Asn Pro Gly Glu Thr Arg

1269 1296
 GGG CCC TGC TTC CTG GCC GGA GAC GGC CGC GCC AGC GAG GTC CCC TCC CTG ACG
 Gly Pro Cys Phe Leu Ala Gly Asp Gly Arg Ala Ser Glu Val Pro Ser Leu Thr

1323 1350
 GCA CTG CAC ACG CTG TGG CTG CGC GAG CAC AAC CGC CTG GCC GCG GCG CTC AAG
 Ala Leu His Thr Leu Trp Leu Arg Glu His Asn Arg Leu Ala Ala Ala Leu Lys

1377 1404
 GCC CTC AAT GCG CAC TGG AGC GCG GAC GCC GTG TAC CAG GAG GCG CGC AAG GTC
 Ala Leu Asn Ala His Trp Ser Ala Asp Ala Val Tyr Gln Glu Ala Arg Lys Val

1431 1458
 GTG GGC GCT CTG CAC CAG ATC ATC ACC CTG AGG GAT TAC ATC CCC AGG ATC CTG
 Val Gly Ala Leu His Gln Ile Ile Thr Leu Arg Asp Tyr Ile Pro Arg Ile Leu

FIG. 7C**SUBSTITUTE SHEET**

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1485 1512
GGA CCC GAG GCC TTC CAG CAG TAC GTG GGT CCC TAT GAA GGC TAT GAC TCC ACC
Gly Pro Glu Ala Phe Gln Gln Tyr Val Gly Pro Tyr Glu Gly Tyr Asp Ser Thr

1539 1566
GCC AAC CCC ACT GTG TCC AAC GTG TTC TCC ACA GCC GCC TTC CGC TTC GGC CAT
Ala Asn Pro Thr Val Ser Asn Val Phe Ser Thr Ala Ala Phe Arg Phe Gly His

x

1593 1620
GCC ACG ATC CAC CCG CTG GTG AGG AGG CTG GAC GCC AGC TTC CAG GAG CAC CCC
Ala Thr Ile His Pro Leu Val Arg Arg Leu Asp Ala Ser Phe Gln Glu His Pro

1647 1674
GAC CTG CCC GGG CTG TGG CTG CAC CAG GCT TTC TTC AGC CCA TGG ACA TTA CTC
Asp Leu Pro Gly Leu Trp Leu His Gln Ala Phe Phe Ser Pro Trp Thr Leu Leu

1701 1728
CGT GGA GGT GGT TTG GAC CCA CTA ATA CGA GGC CTT CTT GCA AGA CCA GCC AAA
Arg Gly Gly Gly Leu Asp Pro Leu Ile Arg Gly Leu Leu Ala Arg Pro Ala Lys

1755 1782
CTG CAG GTG CAG GAT CAG CTG ATG AAC GAG GAG CTG ACG GAA AGG CTC TTT GTG
Leu Gln Val Gln Asp Gln Leu Met Asn Glu Glu Leu Thr Glu Arg Leu Phe Val

1809 1836
CTG TCC AAT TCC AGC ACC TTG GAT CTG GCG TCC ATC AAC CTG CAG AGG GGC CGG
Leu Ser Asn Ser Ser Thr Leu Asp Leu Ala Ser Ile Asn Leu Gln Arg Gly Arg

x

1863 1890
GAC CAC GGG CTG CCA GGT TAC AAT GAG TGG AGG GAG TTC TGC GGC CTG CCT CGC
Asp His Gly Leu Pro Gly Tyr Asn Glu Trp Arg Glu Phe Cys Gly Leu Pro Arg

1917 1944
CTG GAG ACC CCC GCT GAC CTG AGC ACA GCC ATC GCC AGC AGG AGC GTG GCC GAC
Leu Glu Thr Pro Ala Asp Leu Ser Thr Ala Ile Ala Ser Arg Ser Val Ala Asp

FIG. 7D

SUBSTITUTE SHEET

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1971 1998
AAG ATC CTG GAC TTG TAC AAG CAT CCT GAC AAC ATC GAT GTC TGG CTG GGA GGC
Lys Ile Leu Asp Leu Tyr Lys His Pro Asp Asn Ile Asp Val Trp Leu Gly Gly

2025 2052
TTA GCT GAA AAC TTC CTC CCC AGG GCT CGG ACA GGG CCC CTG TTT GCC TGT CTC
Leu Ala Glu Asn Phe Leu Pro Arg Ala Arg Thr Gly Pro Leu Phe Ala Cys Leu

2079 2106
ATT GGG AAG CAG ATG AAG GCT CTG CGG GAC GGT GAC TGG TTT TGG TGG GAG AAC
Ile Gly Lys Gln Met Lys Ala Leu Arg Asp Gly Asp Trp Phe Trp Trp Glu Asn

2133 2160
AGC CAC GTC TTC ACG GAT GCA CAG AGG CGT GAG CTG GAG AAG CAC TCC CTG TCT
Ser His Val Phe Thr Asp Ala Gln Arg Arg Glu Leu Glu Lys His Ser Leu Ser

2187 2214
CGG GTC ATC TGT GAC AAC ACT GGC CTC ACC AGG GTG CCC ATG GAT GCC TTC CAA
Arg Val Ile Cys Asp Asn Thr Gly Leu Thr Arg Val Pro Met Asp Ala Phe Gln

2241 2268
GTC GGC AAA TTC CCC GAA GAC TTT GAG TCT TGT GAC AGC ATC ACT GGC ATG AAC
Val Gly Lys Phe Pro Glu Asp Phe Glu Ser Cys Asp Ser Ile Thr Gly Met Asn

2295 2322
CTG GAG GCC TGG AGG GAA ACC TTT CCT CAA GAC GAC AAG TGT GGC TTC CCA GAG
Leu Glu Ala Trp Arg Glu Thr Phe Pro Gln Asp Asp Lys Cys Gly Phe Pro Glu

2349 2376
AGC GTG GAG AAT GGG GAC TTT GTG CAC TGT GAG GAG TCT GGG AGG CGC GTG CTG
Ser Val Glu Asn Gly Asp Phe Val His Cys Glu Glu Ser Gly Arg Arg Val Leu

2403 2430
GTG TAT TCC TGC CGG CAC GGG TAT GAG CTC CAA GGC CGG GAG CAG CTC ACT TGC
Val Tyr Ser Cys Arg His Gly Tyr Glu Leu Gln Gly Arg Glu Gln Leu Thr Cys

2457 2484
ACC CAG GAA GGA TGG GAT TTC CAG CCT CCC CTC TGC AAA GAT GTG AAC GAG TGT
Thr Gln Glu Gly Trp Asp Phe Gln Pro Pro Leu Cys Lys Asp Val Asn Glu Cys

FIG. 7E**SUBSTITUTE SHEET**

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2511 2538
GCA GAC GGT GCC CAC CCC CCC TGC CAC GCC TGT GCG AGG TGC AGA AAC ACC AAA
Ala Asp Gly Ala His Pro Pro Cys His Ala Ser Ala Arg Cys Arg Asn Thr Lys

2565 2592
GGC GGC TTC CAG TGT CTC TGC GCG GAC CCC TAC GAG TTA GGA GAC GAT GGG AGA
Gly Gly Phe Gln Cys Leu Cys Ala Asp Pro Tyr Glu Leu Gly Asp Asp Gly Arg

2619 2646
ACC TGC GTA GAC TCC GGG AGG CTC CCT CGG GTG ACT TGG ATC TCC ATG TCG CTG
Thr Cys Val Asp Ser Gly Arg Leu Pro Arg Val Thr Trp Ile Ser Met Ser Leu

2673 2700
GCT GCT CTG CTG ATC GGA GGC TTC GCA GGT CTC ACC TCG ACG GTG ATT TGC AGG
Ala Ala Leu Leu Ile Gly Gly Phe Ala Gly Leu Thr Ser Thr Val Ile Cys Arg

2727 2754
TGG ACA CGC ACT GGC ACT AAA TCC ACA CTG CCC ATC TCG GAG ACA GGC GGA GGA
Trp Thr Arg Thr Gly Thr Lys Ser Thr Leu Pro Ile Ser Glu Thr Gly Gly Gly

2781 2808
ACT CCC GAG CTG AGA TGC GGA AAG CAC CAG GCC GTA GGG ACC TCA CCG CAG CGG
Thr Pro Glu Leu Arg Cys Gly Lys His Gln Ala Val Gly Thr Ser Pro Gln Arg

2835 2862
GCC GCA GCT CAG GAC TCG GAG CAG GAG AGT GCT GGG ATG GAA GGC CGG GAT ACT
Ala Ala Ala Gln Asp Ser Glu Gln Glu Ser Ala Gly Met Glu Gly Arg Asp Thr

2889 2916
CAC AGG CTG CCG AGA GCC CTC TGA GGG CAA AGT GGC AGG ACA CTG CAG AAC AGC
His Arg Leu Pro Arg Ala Leu ^^^

2943 2970
TTC ATG TTC CCA AAA TCA CCG TAC GAC TCT TTT CCA AAC ACA GGC AAA TCG GAA

2997 3024
ATC AGC AGG ACG ACT GTT TTC CCA ACA CGG GTA AAT CTA GTA CCA TGT CGT AGT

3051
TAC TCT CAG GCA TGG ATG AAT AAA TGT TAT AGC TGC AAA AAA AAA AAA
^^^ ^^^

FIG. 7F**SUBSTITUTE SHEET**

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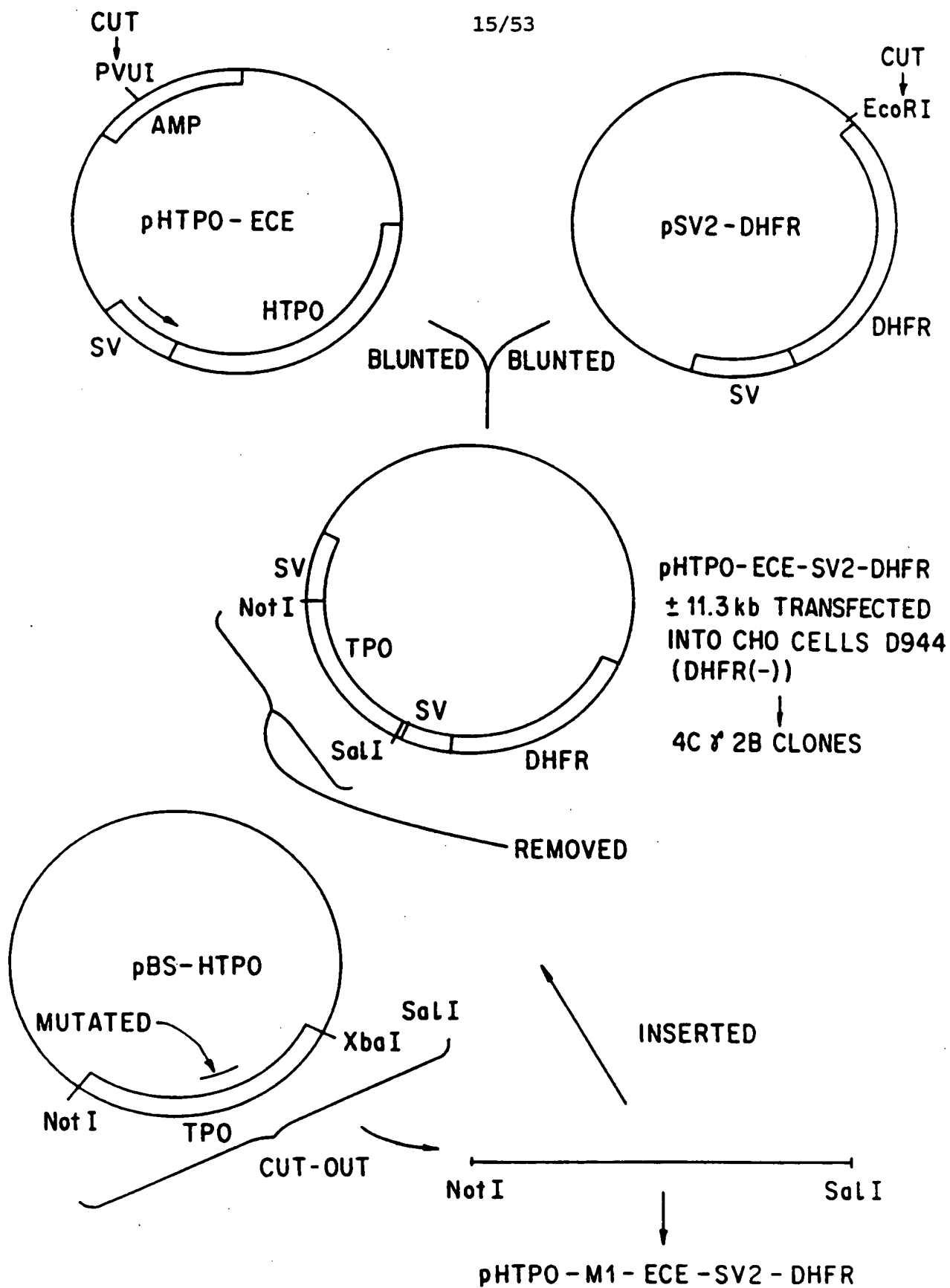


FIG. 9 SUBSTITUTE SHEET

HUMAN THYROID
MICROSOMES

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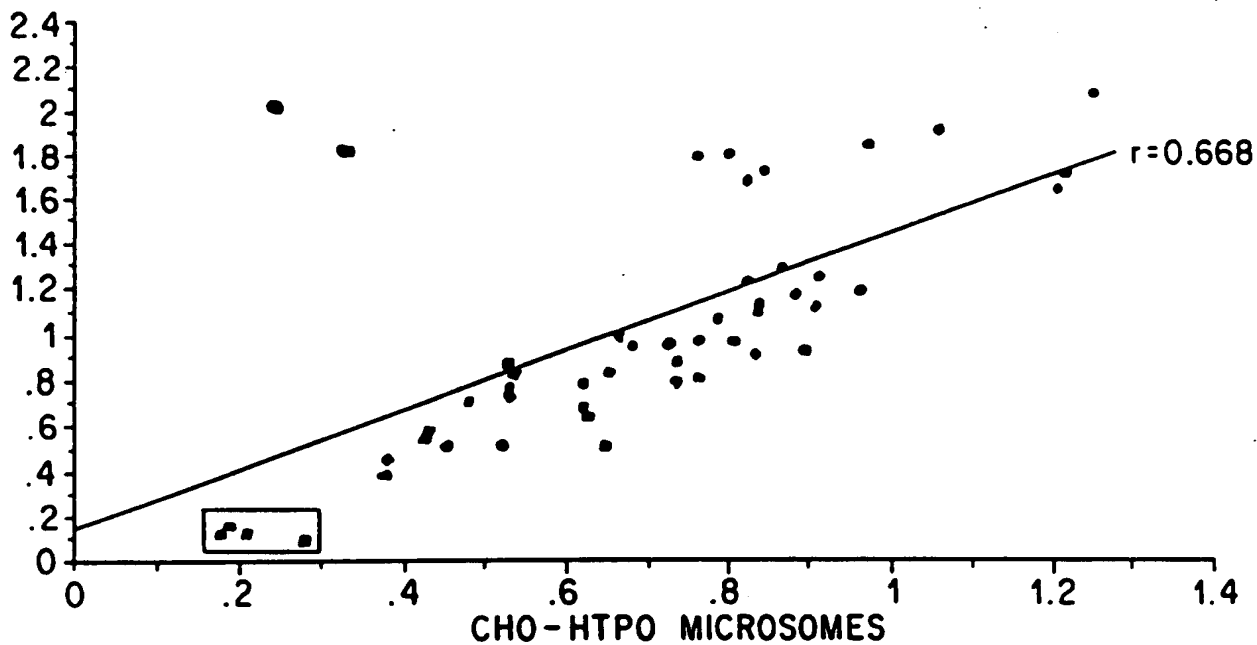


FIG. 10A

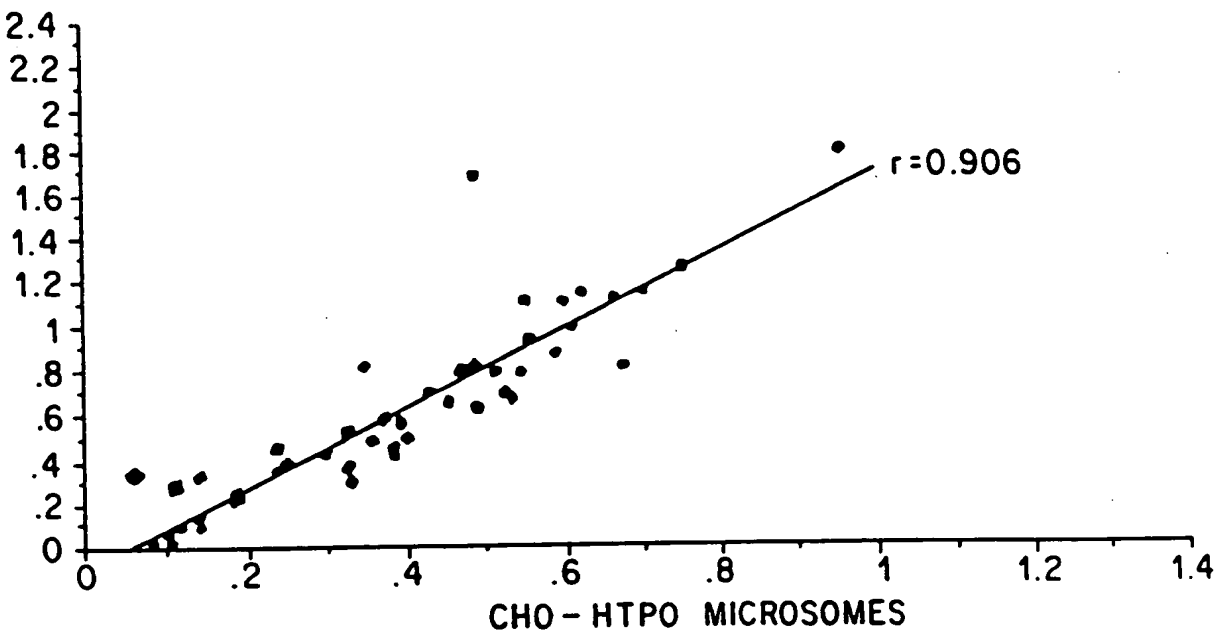
HUMAN THYROID
MICROSOMES

FIG. 10B

SUBSTITUTE SHEET

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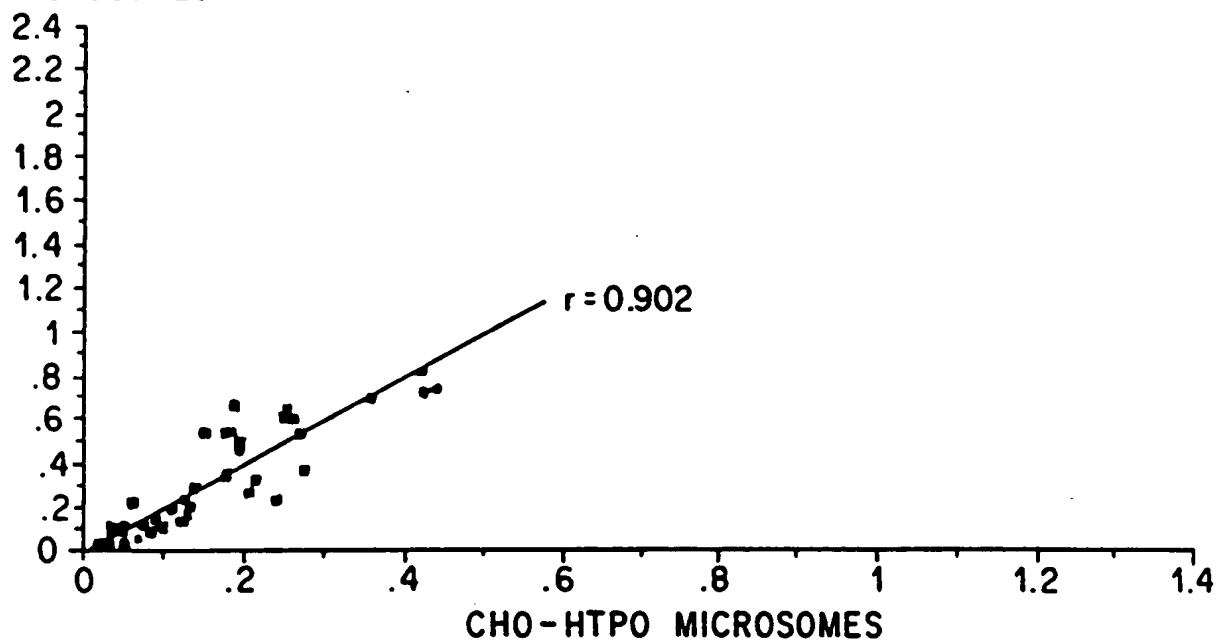
HUMAN THYROID
MICROSOMES

FIG. 10C

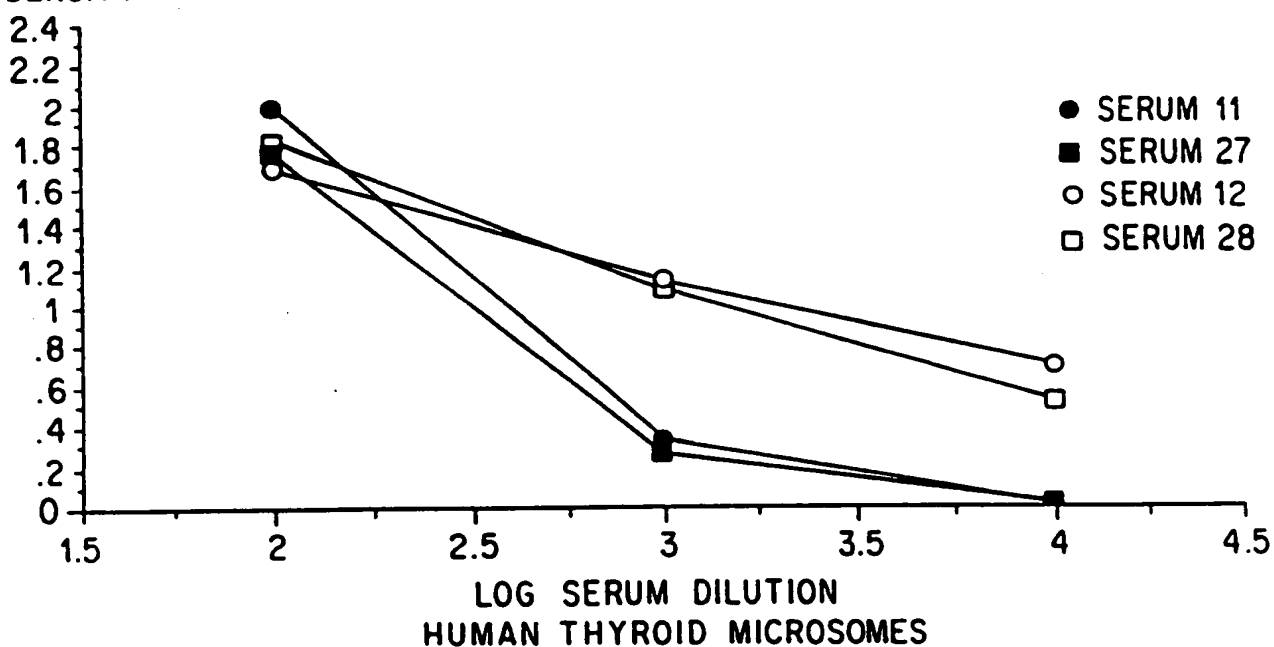
OPTICAL
DENSITY

FIG. 11A

SUBSTITUTE SHEET

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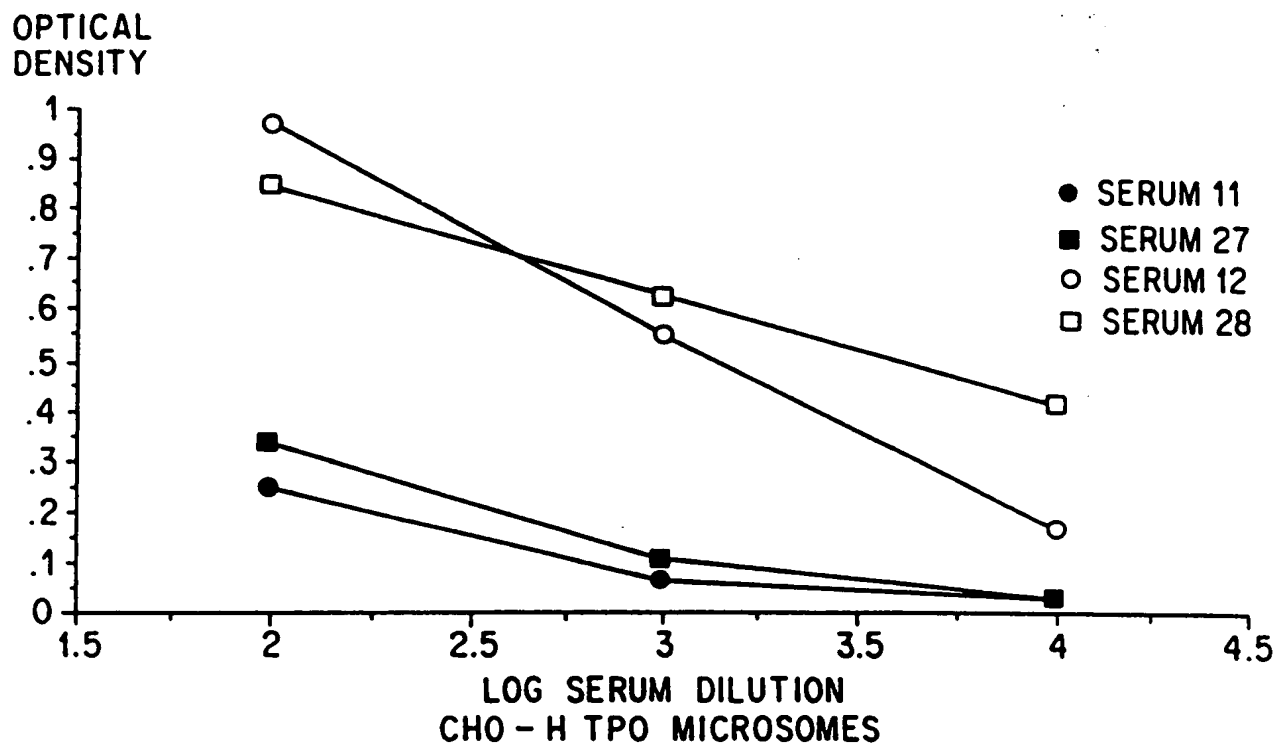
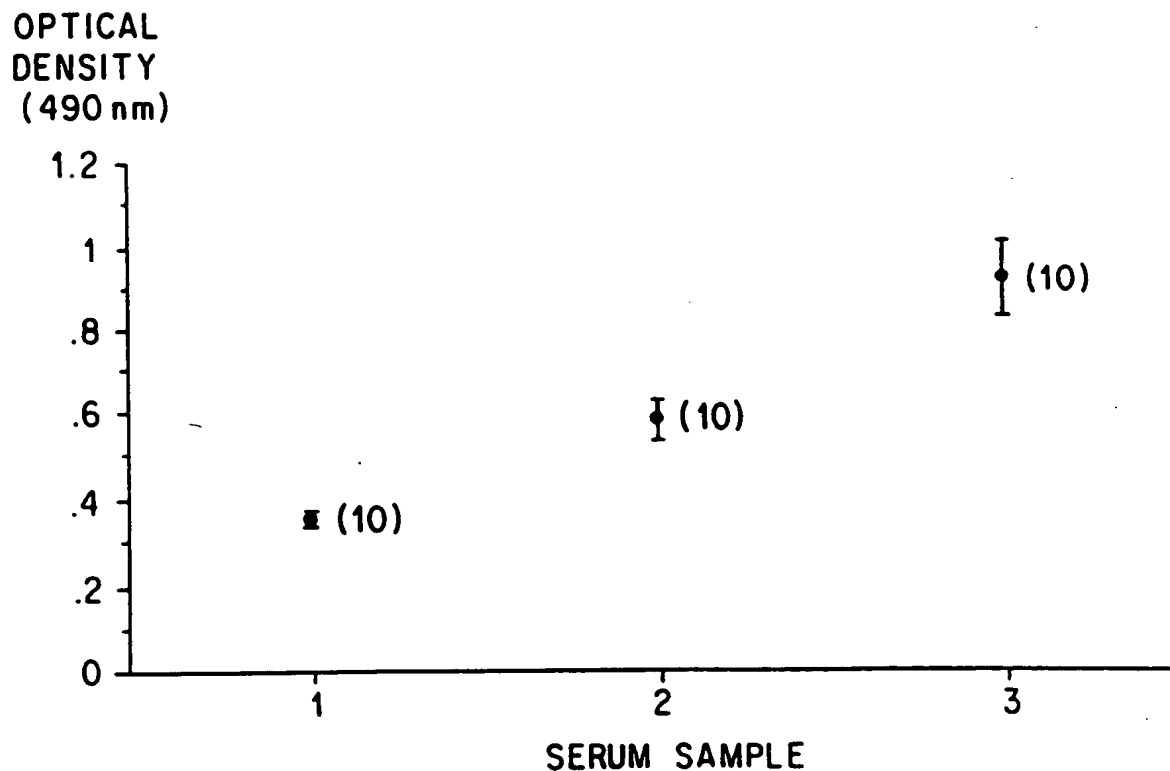
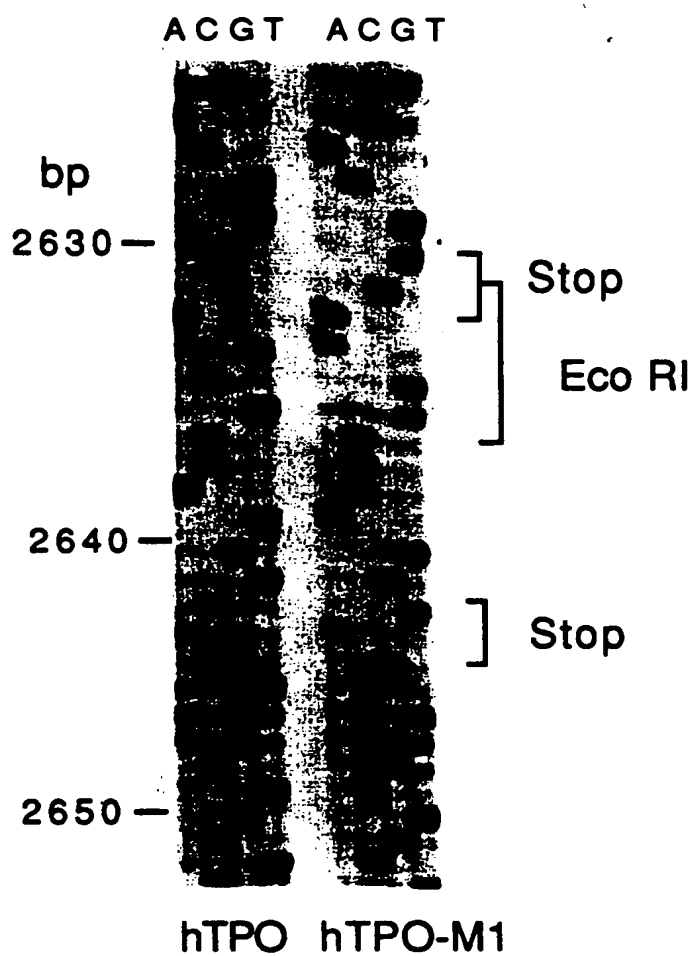


FIG. 11B



**FIG.13**

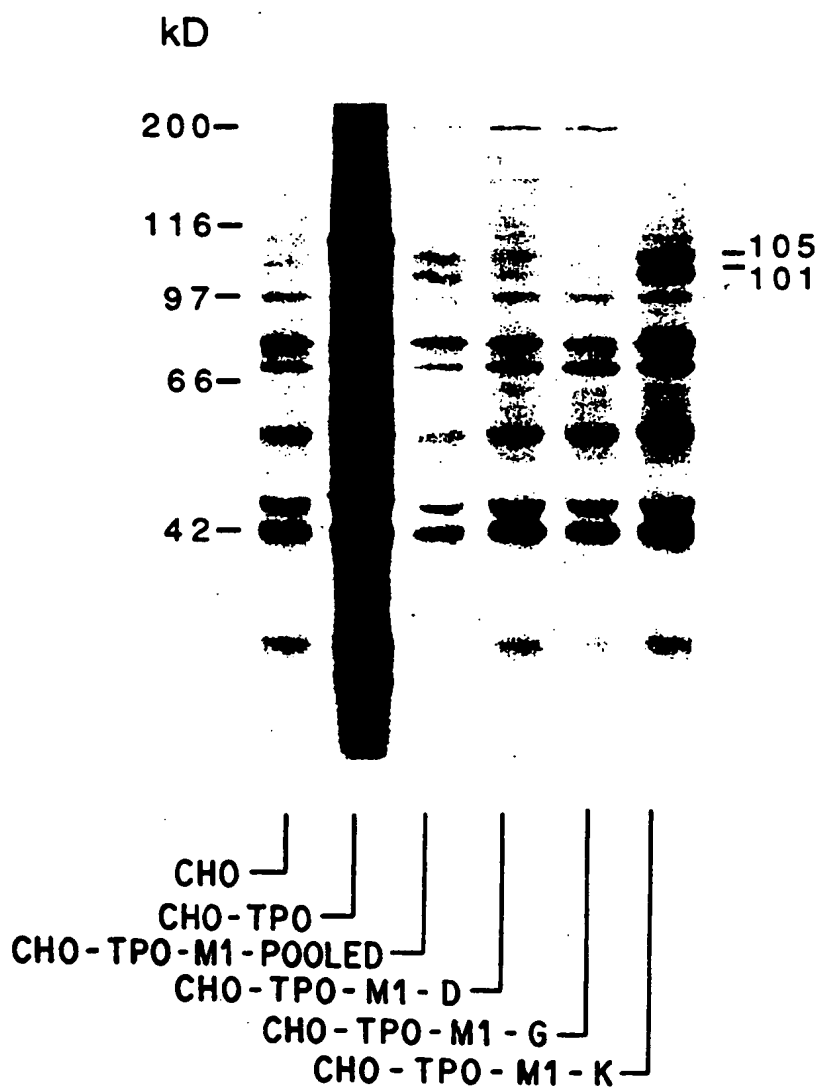


FIG. 14A

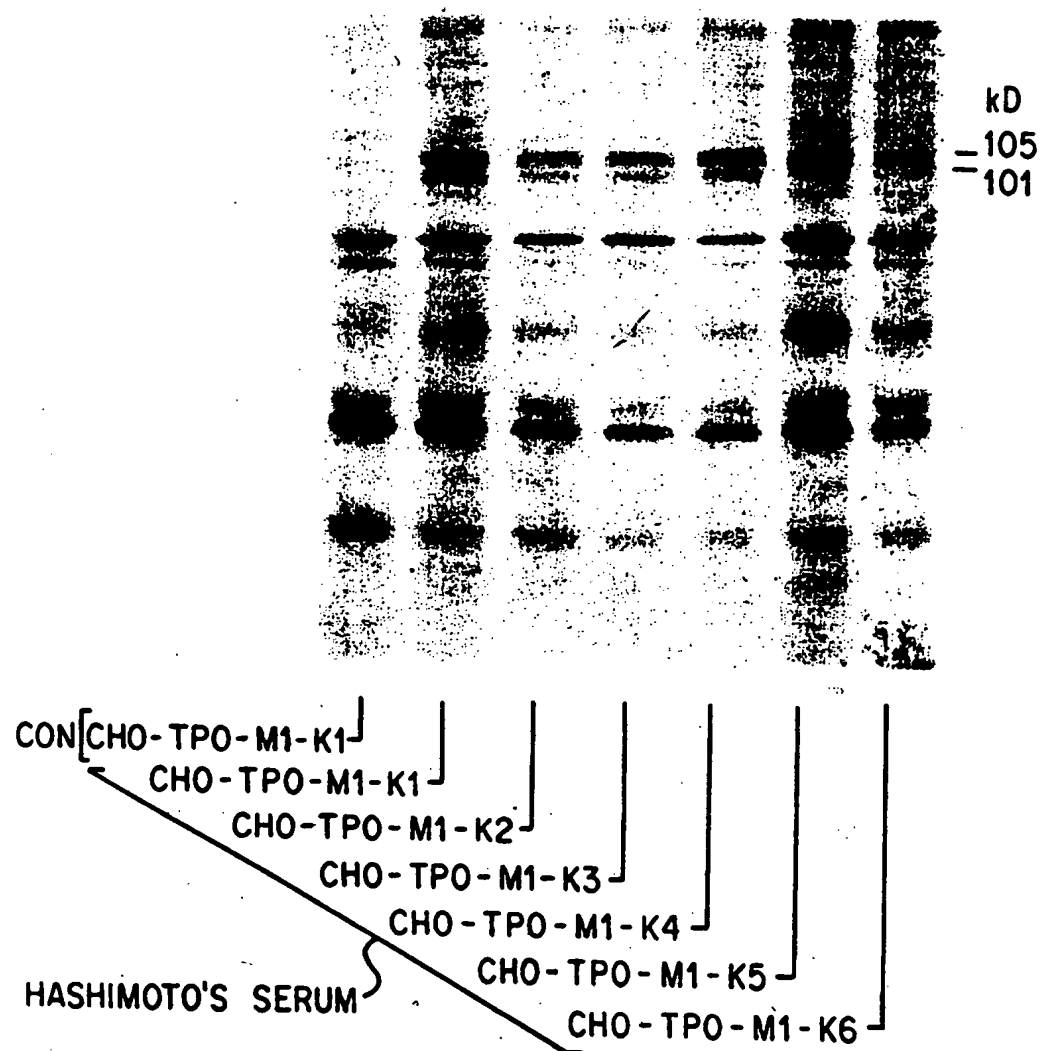


FIG. 14B

SUBSTITUTE SHEET

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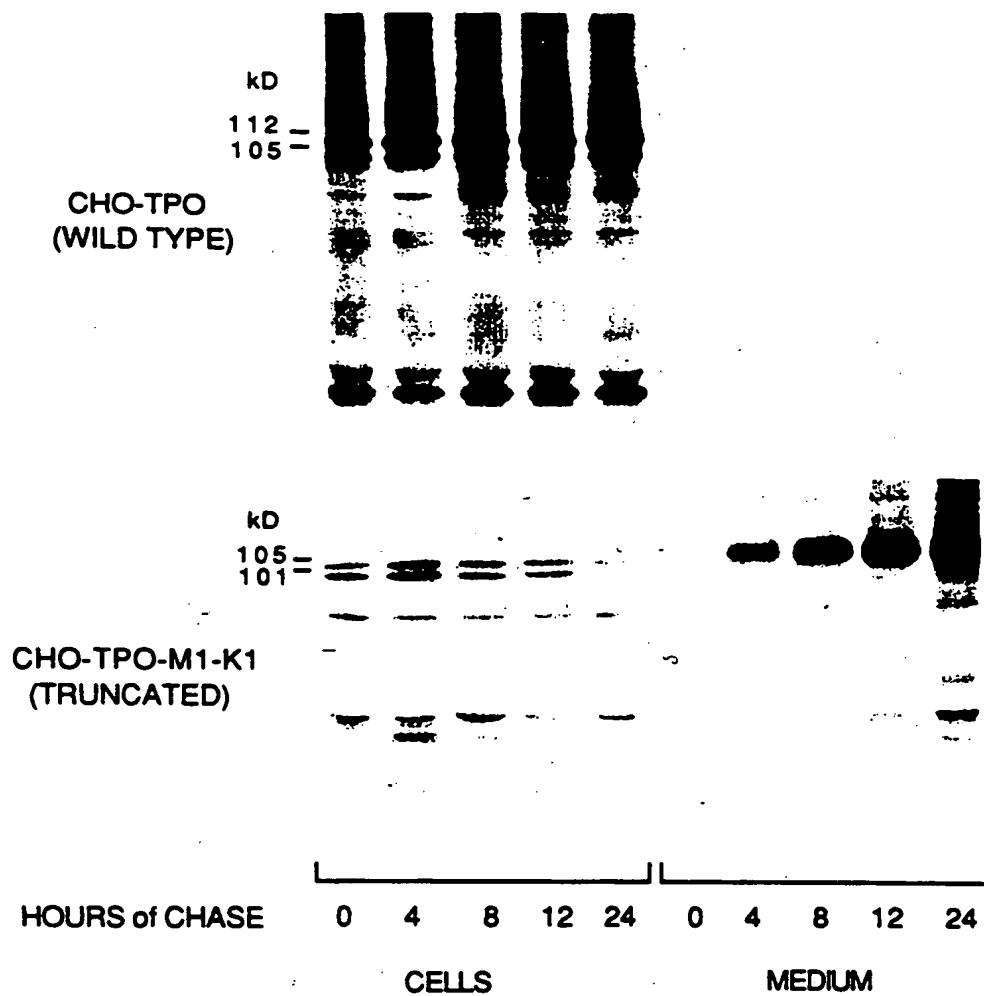


FIG. 15

SUBSTITUTE SHEET

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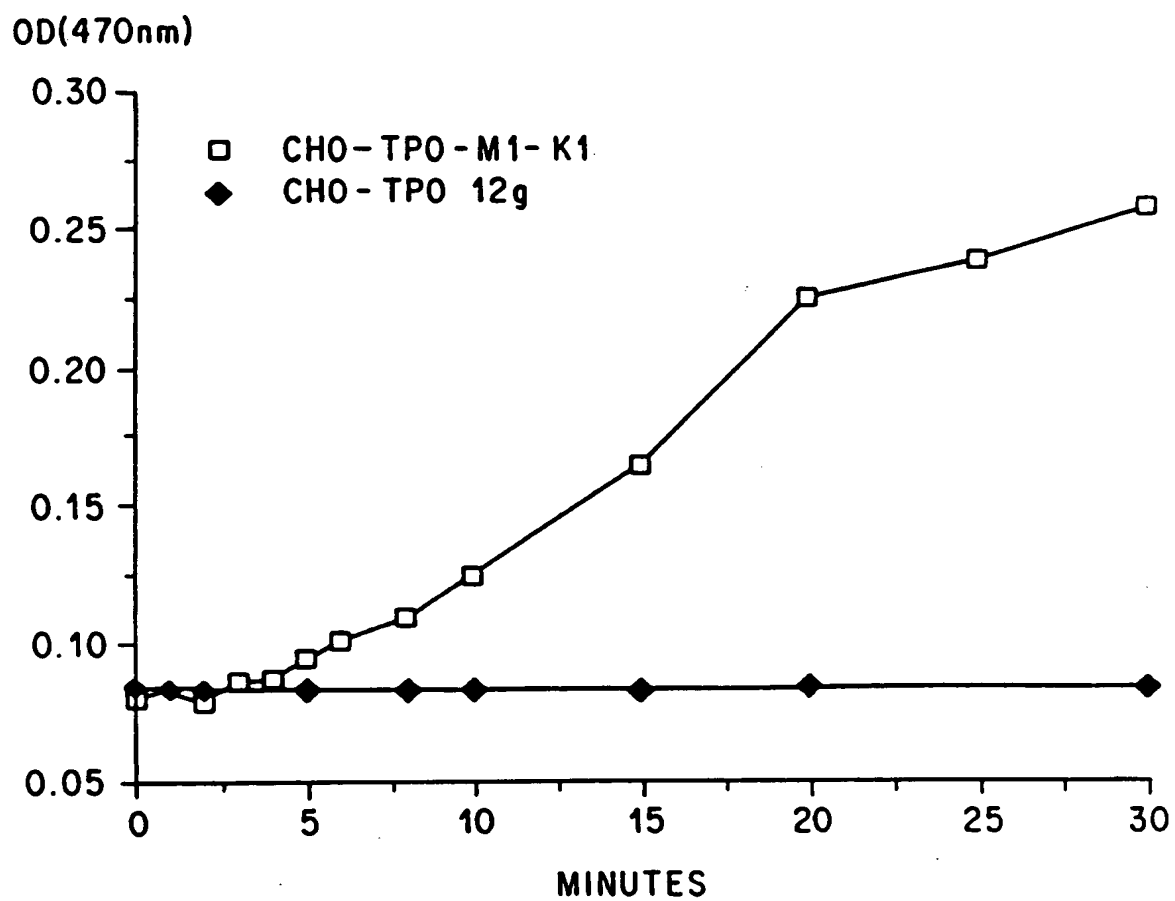


FIG. 16

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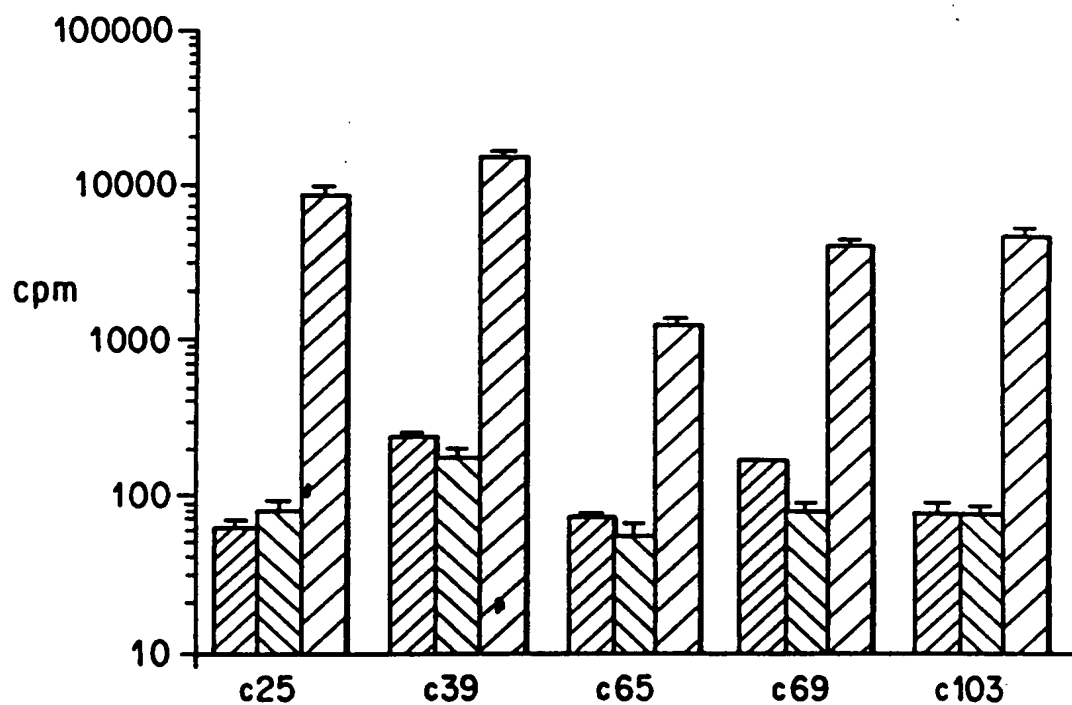


FIG. 17A

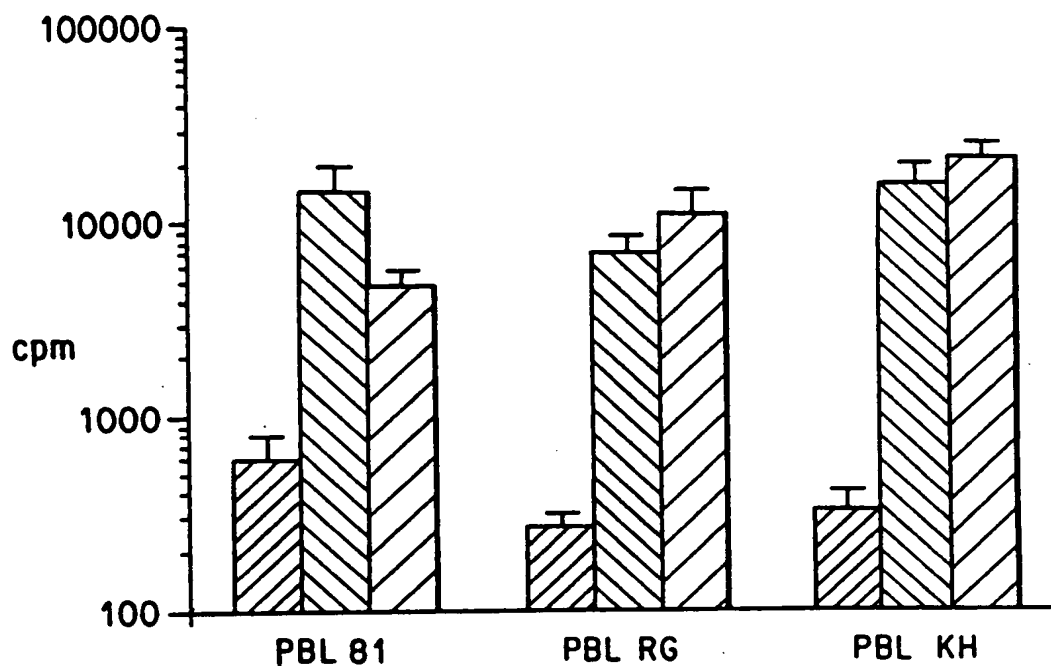


FIG. 17B

SUBSTITUTE SHEET

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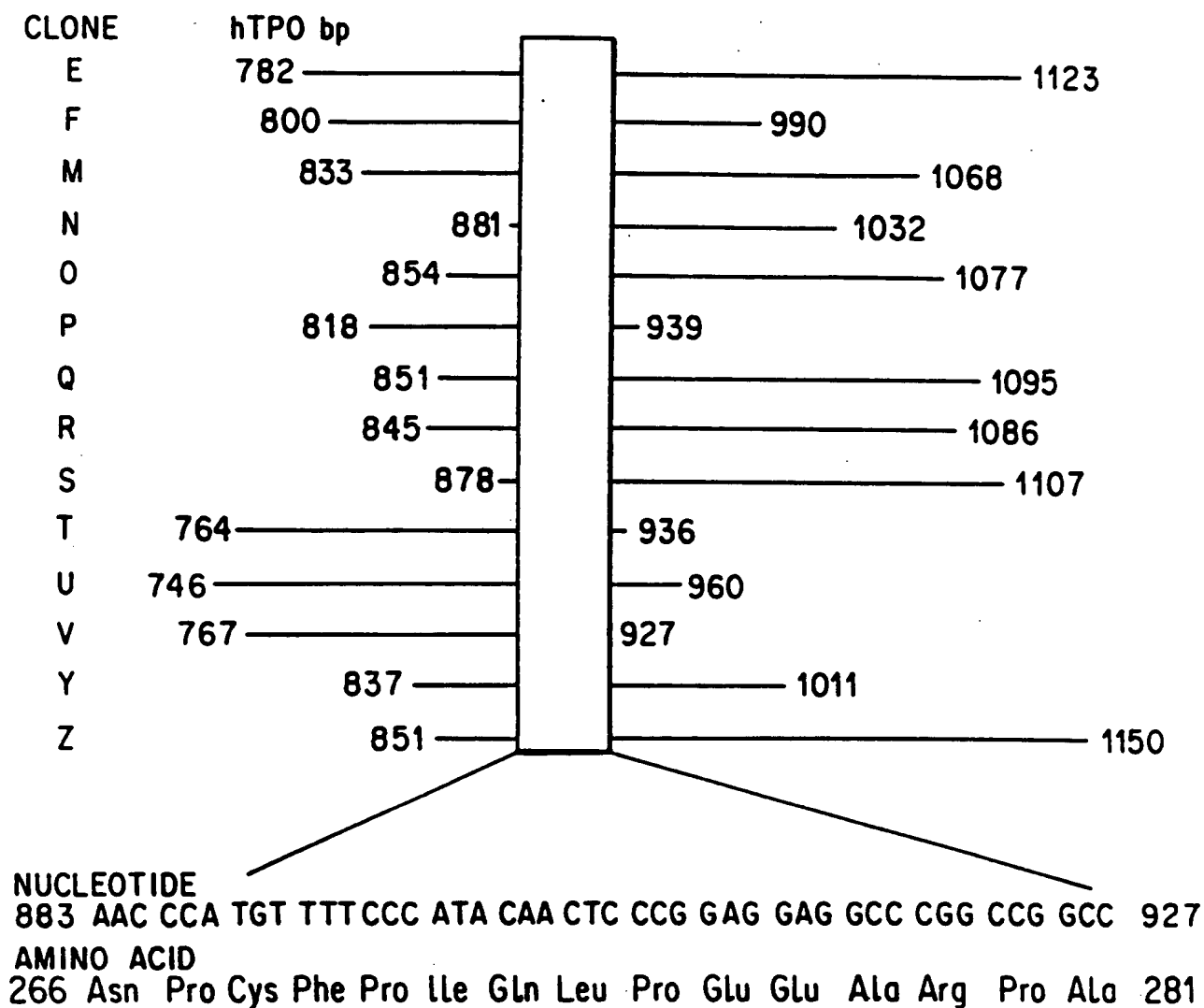
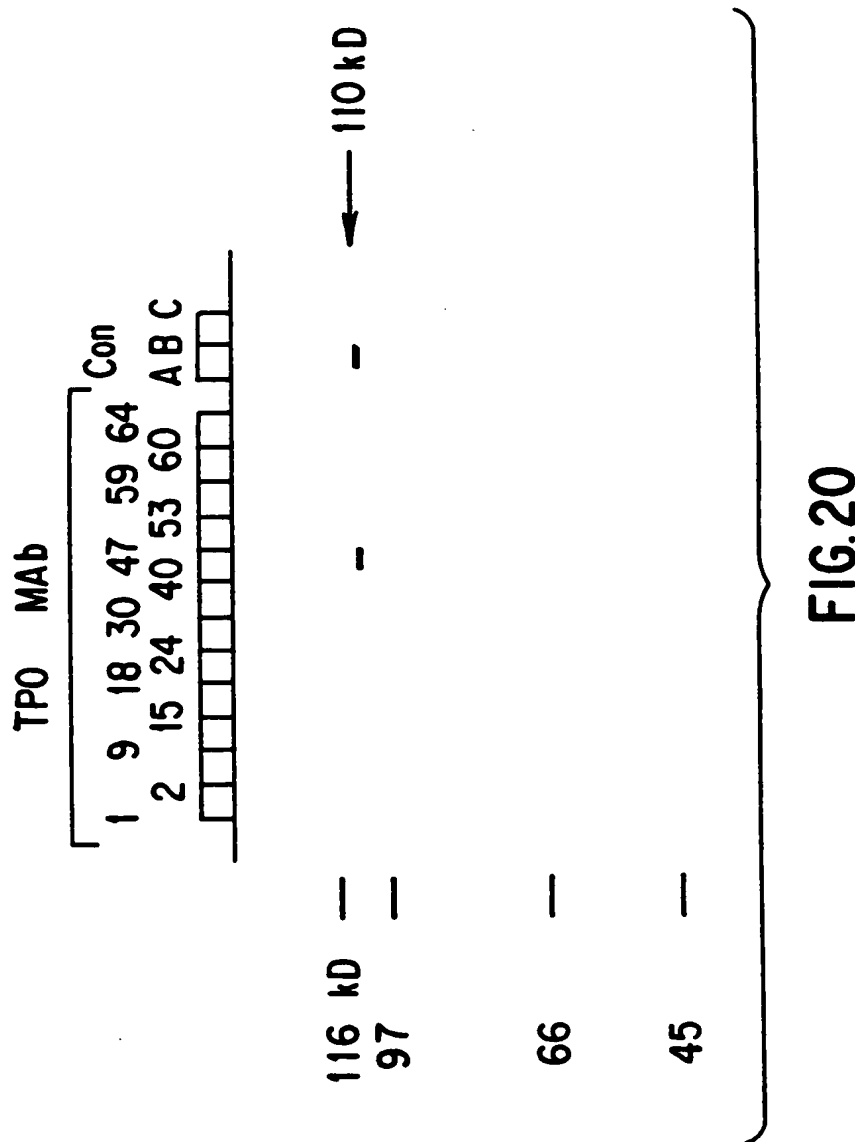


FIG. 18

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SUBSTITUTE SHEET



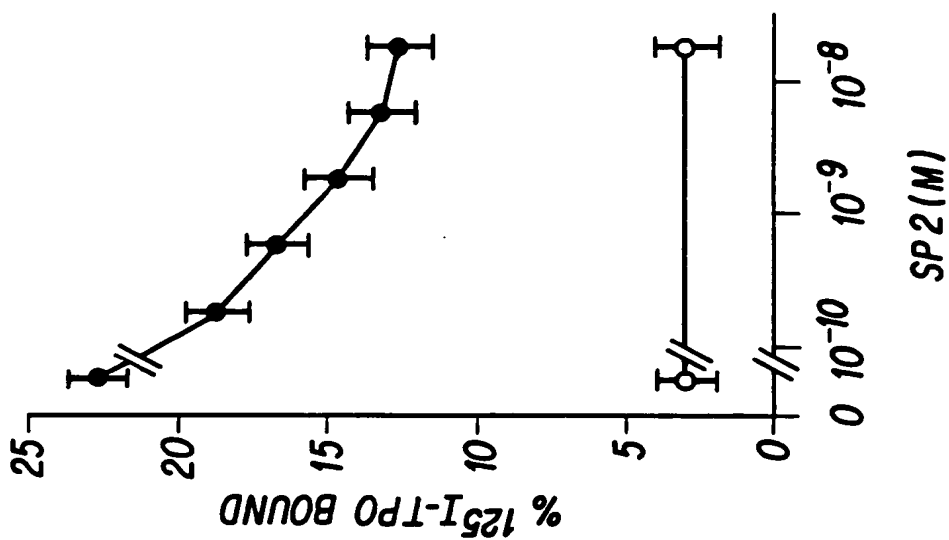


FIG. 28

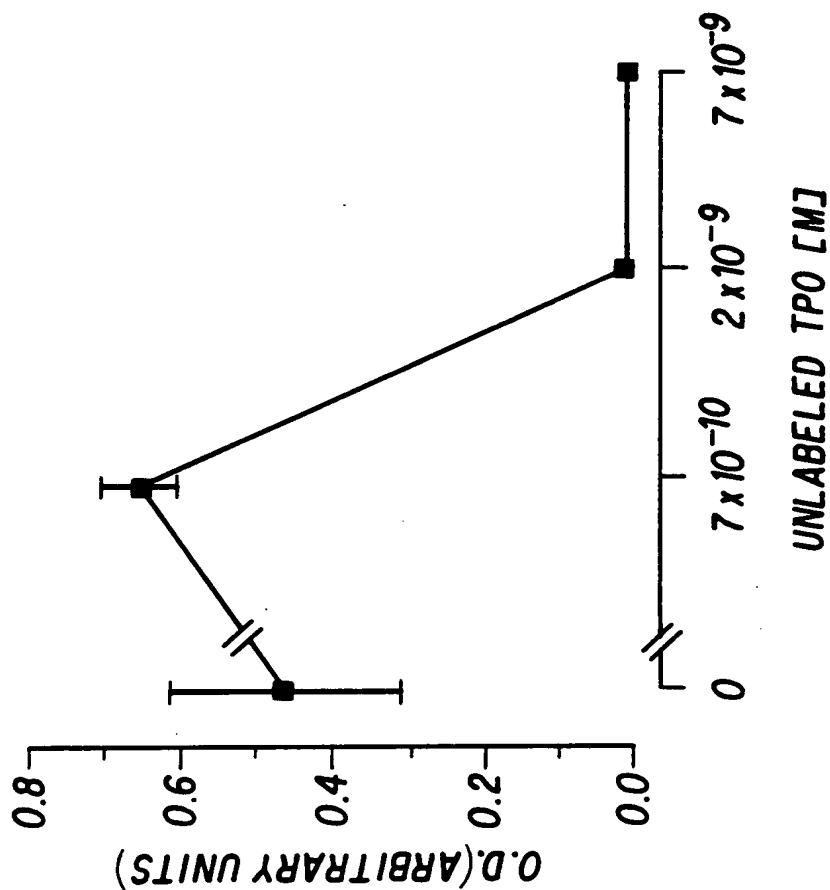


FIG. 21

VH SEGMENT (VHI)

Q V K L L E S G A E V K K P G A S V K V
 CAGGTGAACCTGCTCGAGTCTGGGCTGAGGTGAAGAAGCCTGGGCTCAGTGAAGGTC
 ---CAG---G-GC---C-----T-----
 SP2 1-1 60

S C K A S G Y T F T G H Y M H W V R Q A
 TCCTGCAAGGCTTCTGGATACACCTTCACCGGCACTATATGCACCTGGTGGCAGGCC
 ---T-----
 SP2 1-1 120

CDR1

 P G Q G L E W I G W I S P N R G A T R F
 CCTGGACAAGGCTTGTAGTGGATAGGATGATCAGCCCTAACAGAGGTGCCACAAGGTTT
 ---G-----A-----T-----G-----C-AC-A-
 SP2 1-1 180

CDR2

 A Q K F Q G R V T M T S D T S I N T V Y
 GCACAGAAGTTTCAGGGCAGGGTCACCATGACCGACACGTCCTCATTAACACAGTCTAC
 ---G-----C-G-----C-----
 SP2 1-1 240

M E L S G L R F D D T A V Y Y C A T
 ATGGAGCTGAGCGGCTGAGATTGACGACACGGCCGTGTATTACTGTGCGACA
 ---AAG---C-----G-----
 SP2 1-1

SUBSTITUTE SHEET

FIG. 22

Cancel
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D SEGMENT

CDR3

 T R T A Y Y G M D
 SP2 ACACGCACGGCCTACTACGGTATGGAC

JH SEGMENT (JH3)

SP2GTCTGGGGCCCAAGGACCAACGGTCACCGTCTCTTCA
 JH3 ATGCTTTTGAT-----A-T-----R L G P R D H G H R L F

FIG. 22 (CONT.)

*Cancel
Per
F*

VL SEGMENT (VK1)

E L V M T Q S P S L S A S E G D T V T
 SP2 GAGCTCGTGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGAGACACAGTCACC 60
 KLVJ --CA--CA-----C-----TA-----G-----

CDR1

I T C R A S E N I S R Y S N W Y Q Q Q P
 SP2 ATCACTTGCCGGCAAGTGAGAAATATTAGCAGGTATTCAAAATTGGTATCAGCAGCAACCA 120
 KLVJ -----C-----GC-----T-AC-----T-----A-----

CDR2

G K A P K L L I S A A S T L Q S G V P S
 SP2 GGGAAAGCCCTAAACTCCTGATCTCTGCTGCATCCACTTTACAAAGTGGGTCCCATCA 180
 KLVJ -----G-----A-----G-----G-----

R F S G S G S G T H F T L T I N S L Q P
 SP2 AGGTCAGTGGCAGTGGATCTGGGACACATTTCACTCTCACTCAACAGTCTGCAACCT 240
 KLVJ -----G-----G-----G-----G-----

CDR3

G D F A T Y Y C Q Q T Y S S P F
 SP2 GGAGATTTGCAACTTACTACTGTCAACAGACTTACAGTTCCTCCCGTTC
 KLVJ -A-----G-----A-----ACC-T

J SEGMENT (JK2)

T F G Q G T K L E I K R T
 SP2 ACTTTGGCCAGGGACCAAGCTGGAGATCAACGAACT
 KV312-----

FIG. 23

SUBSTITUTE SHEET

Cancel
Per
F

KLVJ CA.....C.....TA..... 50
 VK-SP2 GC.....T.....AG..... 50
 VK-SP4 GC.....C.....TG..... 50
 VK-SP5 GC.....C.....TA..... 50
 Consensus GA--TCGTGA TGACCCAGTC TCCATC-TCC CTGTCTGCAT CTG--GGAGA 50

KLVJ G.....C.....GCA..A.T..AC....T.. 100
 VK-SP2 C.....C.....G.....ATA..A.C..GG....C.. 100
 VK-SP4 G.....C.....C.....CCG..G.C..CC....T.. 100
 VK-SP5 G.....G.....C.....ACA..G.C..AA....T.. 100
 Consensus CA-AGTCACC ATCA-TTGCC GGGCAAGT-A GA---TT-G- A--TATT-AA 100

CDR1

KLVJ A...GA.A...A.....A.G.....G..C.A.GC. 150
 VK-SP2 A...GC.A...A.....A.A.....G..C.C.GC. 150
 VK-SP4 A...AA.A...G.....A.A.....C..C.A.AC. 150
 VK-SP5 G...GA.G...A.....G.G.....G..A.A.GG. 150
 Consensus ATTGGTATC- GCA--A-CCA GGG-AAGCCC CT-A-CTCCT -AT-T-T--T 150

**

FIG. 24

**

*Cancel
Per
#*

KLVJ G.....G.. .G..... .T.A.. 200
 VK-SP2 G.....C.. .A..... .T.A.. 200
 VK-SP4 G.....C.. .G..... .G.C.. 200
 VK-SP5 A.....C.. .G..... .T.G.. 200
 Consensus -CATCCA-TT T-CAAAGTGG GGTCCCATCA AGGTTCAAG-G GCAGTGG-TC 200

CDR2

KLVJG..G...A..... 250
 VK-SP2C..A...G..... 250
 VK-SP4G..G...A..... 250
 VK-SP5G..G...A..... 250
 Consensus TGGGACA-AT TTCACCTCTCA CCATCA-CAG TCTGCAACCT G-AGATTTTG 250

KLVJG.....A ...ACCT 288
 VK-SP2C.....T ...CGTT 288
 VK-SP4G.....A ...CGTG 288
 VK-SP5G.....A ...CGTG 288
 Consensus CAACTTACTA CTGTCAACAG A-TTACAGT- CCC---- 288

CDR3

FIG. 24 (CONT.)

SUBSTITUTE SHEET

Cancel
 Per
 F

KLVJ	DI.....S.S N.....A	50
VK-SP2E..T..EN.S R.S.....Q.SA	50
VK-SP4TVG T.....E.....T	50
VK-SP5S.....N.G K.....R....E.....G	50
Consensus	ELVMTQSPSS LSASVGDRVT	ITCRASQ.I. .YLNWYQKP	GKAPKLLIY.	50

CDR1

*

KLVJ	S.....	96
VK-SP2H.....N....	G.....T..S.V	96
VK-SP4R.....V	96
VK-SP5	T.....V	96
Consensus	ASTLQSGVPS RFGSGSGTD	FTLTSSLPQ EDFATYYCQQ	SYSTPP	96

CDR2

CDR3

FIG. 25

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J-KV312	..T..T....	.G.....	.C....G....	39
JK-SP2	..T..T....	.G.....	.C....G....	39
JK-SP4/5	..G..C....	.A.....	.G....A....	39
Consensus	AC-TT-GGCC	A-GGGACCAA	G-TGGA-ATC	AAACGAACT	39

J-KV312	13
JK-SP2	13
JK-SP4/5V....	13
Consensus	TFGQGTKLEI KRT	13

FIG. 26

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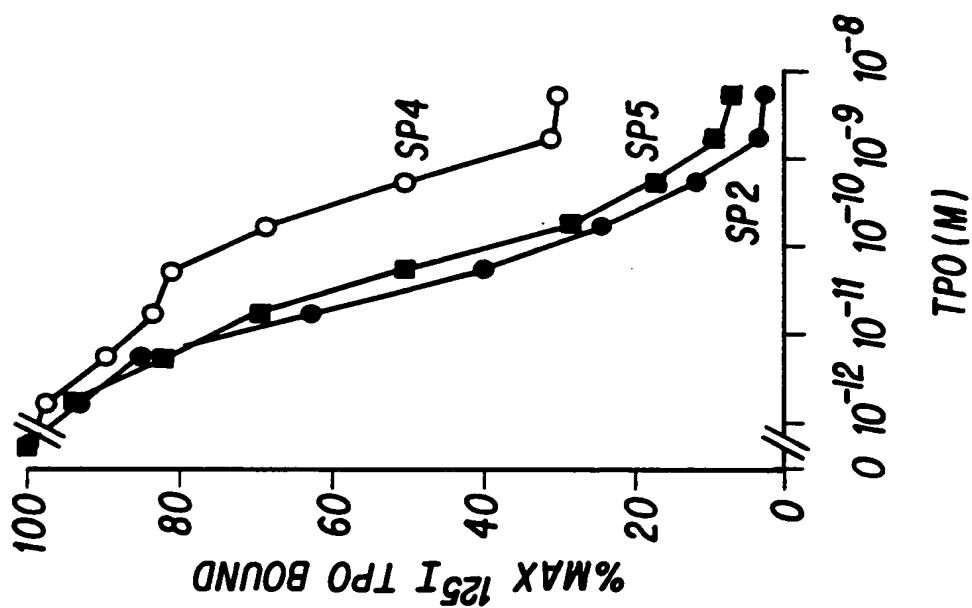


FIG. 27B

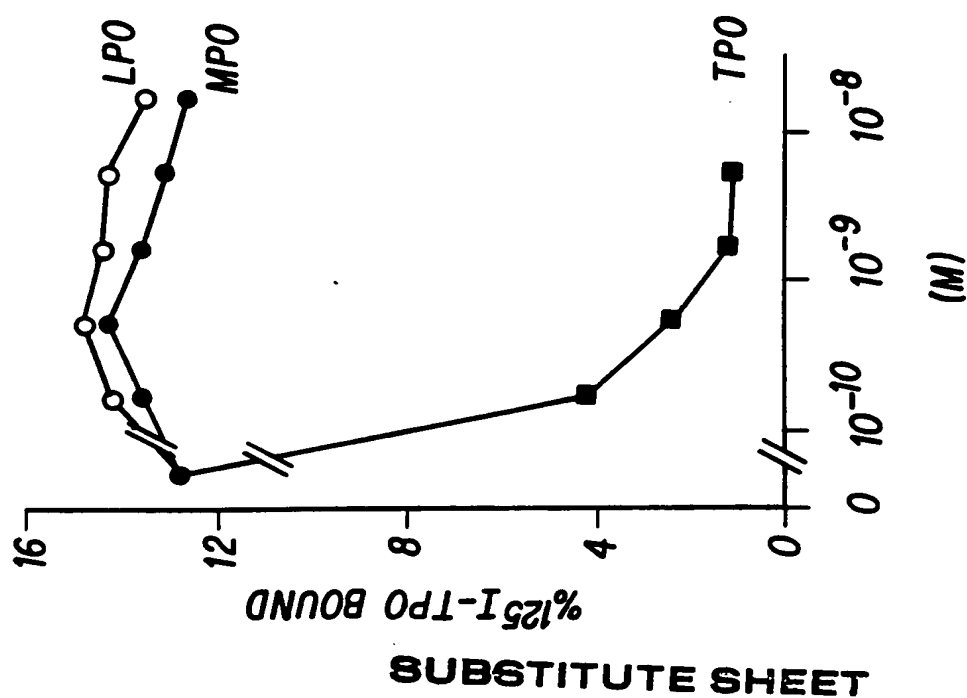


FIG. 27A

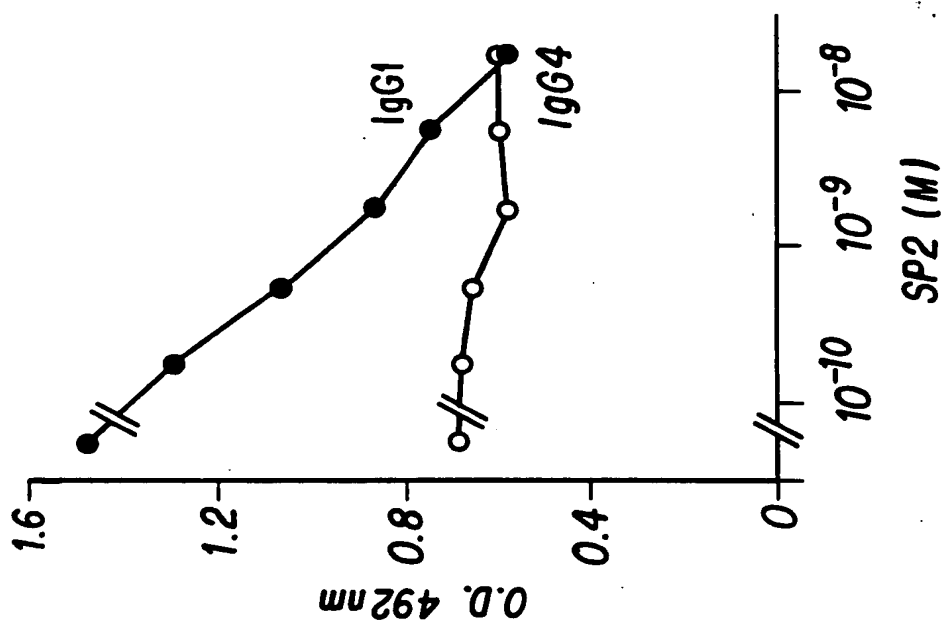


FIG. 29B

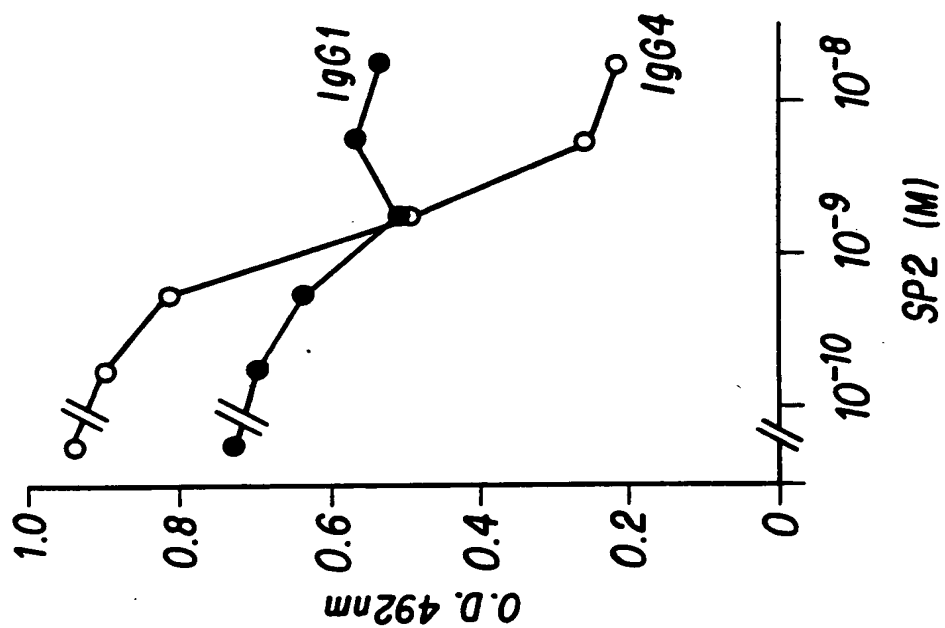


FIG. 29A

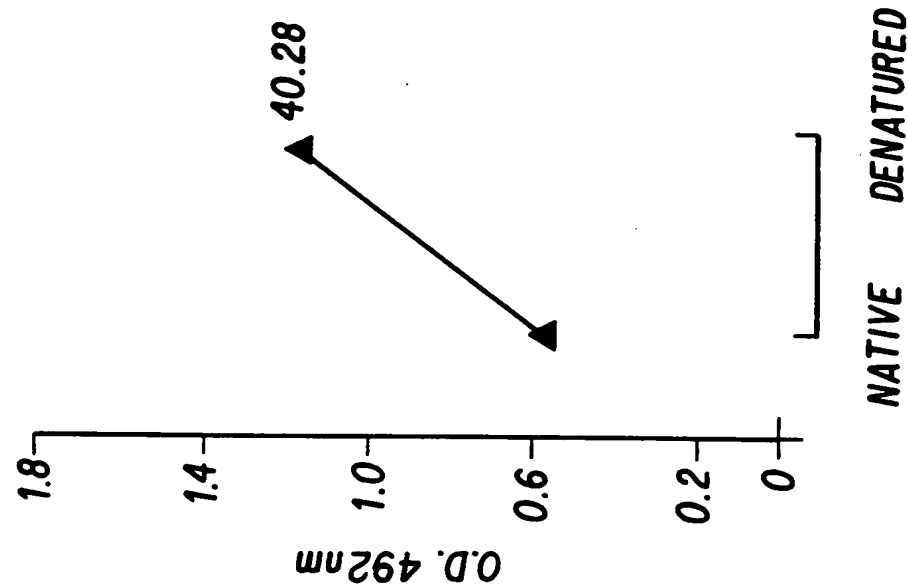


FIG. 30A

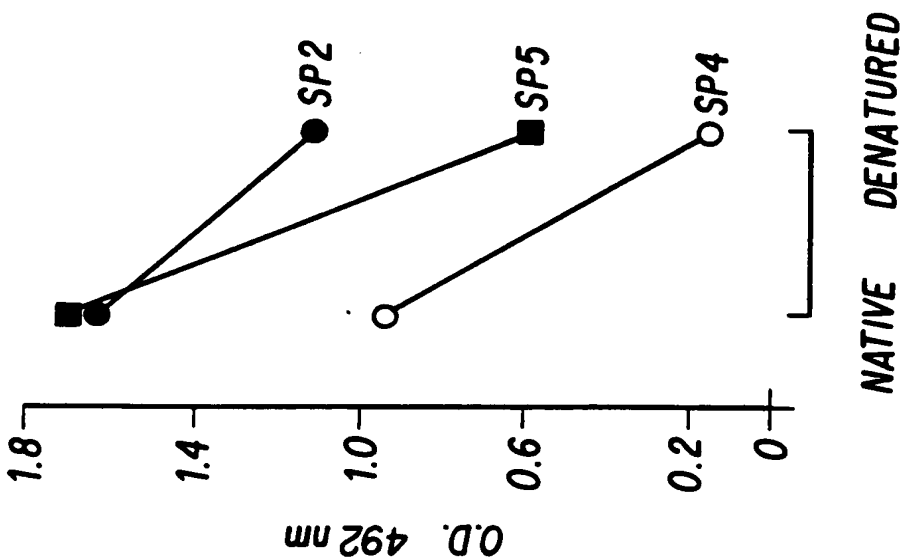


FIG. 30B

Consensus CAGGTG-A-C TG-T--AGTC TGGGGCTGAG -TGAA-AA-C CTGGGGCCCTC 50
 hv1L1C.G. ..G.GC..... G....C..G. 50
 SP4.6A.A. ..C.CG..... T....G..C. 50

Consensus AGTGA-GGTC TCCTGCAAGG CTCTGGA-A CACCTTCA-C G-CTAC-AT- 00
 hv1L1A.....G.C.G....T..A 00
 SP4.6G.....T.A.C..G 00

Consensus T-CACTGGGT GCGACAGGCC CCTGGACAAG GGCTTGAGTG G-TGGGATGG 150
 hv1L1 .G..... .A..... 150
 SP4.6 .T..... .G..... 150

FIG. 31A

0 hv1L1
 SP4.6

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CDR2

Consensus	ATCAACCCTA A-A-TG-TGG CAC-A--TAT -C-CAGAGCT TCCACGGCAG	200
hvl1L1 C.G..G... ..A.AC... G.A.....	200
SP4.6 G.A..C... ..G.GA... T.C.....	200

Consensus	GGTCACCATG ACCAG-GACA CG-CCATCAG C-CAGCCTA- ATGGAGCTGA	250
hvl1L1 G.... .T..... .A.....C	250
SP4.6 A.... .G..... .G.....T	250

Consensus	-CAG-CTGA- ATC-GACGAC ACGGCCGT-T A-TACTGTGC G-GA	294
hvl1L1	G...G....G ...T.....G. .T..... .A..	294
SP4.6	C...C....A ...G.....C. .C..... .C..	294

FIG. 31A (CONT.)

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Consensus	QV-L--SGAE	---PGASV-V	SCKASG-TF-	CDR1	-Y--HWVRQA	PGQGLEW-GW	50
hv1L1	..Q.VQ....	VNK.....K.D..T	G.YM....M..		50
SP4.6	..K.LE....	LKN.....R.Y..N	D.HV....V..		50

CDR2

Consensus	INP---GT-Y	-QKFQGRVTM	TRDT-IS-AY	MEL--L-SDD	TAVYYCAR	98
hv1L1	...NSG..N.	A.....S..T..	...SR.R...	98
SP4.6	...KNA..R.	S.....A..A..	...TS.K...	98

FIG. 31B

SP4.6 GGG GTA GGA GTT GGT ACG TGG GGC CTT
G V G G V G T W G L

FIG. 31C

Cancel Per F

CDR1

Consensus	ELVMTQSPSS	LSASVGDRVT	ITCRASQ-IS	-YLNWYQQKP	GKAPKLLIY-	
KLVD	DI	S..N..	50
SP # 14,15,21,22	S..N.GK..	50
18	E.....	RA..T..	50
20	S..A..	50
12	G.....	S..A..	50
13	T..T..	R.....	50
16	D..R..	50
17,19	E..T..	EN..R.S..	50

CDR2

CDR3

Consensus	ASTLQSGVPS	RFSGSGGTD	FTLTSSLOP	EDFATYYQQ	SYSTP-	
KLVD	..S..	96
SP # 14,15,21,22	T.....	F.....	F.....	96
18	T.....	F.....	F.....	96
20	..S..	96
12	..S..	96
13	G.....	T....	D.....	96
16	..E..	Y.....	96
17,19	H....	G.....	96

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FIG. 32A

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CDR3		TFGQGTKLEI KR	
Consensus	SP #		
21	14, 15, 22	..P..RV.V ..	JK ?
18		..E..E..E..E..	JK2
20		..H...V... ..	JK1
12		..H...V... ..	JK2
13		..E..E..E..E..	
16		..E..E..E..E..	
17, 19		..E..E..E..E..	

FIG. 32B

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